STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 151497

TO: Sumesh Kaushal Location: REM-2B85/2C70 Art Unit: 1636 Wednesday, April 27, 2005 Case Serial Number: 10/735014	From: Barb O'Bryen Location: Biotech-Chem Library Remsen 1a69 Phone: 571-272-2518 barbara.obryen@uspto.gov

Search Notes

sira Search and Information Resources Administration

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 26, 2005, 19:00:41 ; Search time 122 Seconds
(without alignments)
1366.342 Million cell updates/sec

Title: US-10-735-014-83
Perfect score: 2211
Sequence: 1 MFFGGEGSLTYTLVIICFLT.....LRRKRYSRLDYLINGIYVDI 431

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2211	100.0	431	2	AAY17834	Aay17834 Human PRO
2	2211	100.0	431	3	AAB33428	Aab33428 Human PRO
3	2211	100.0	431	3	AAB01325	Aab01325 Human PRO
4	2211	100.0	431	3	AAB34739	Aab34739 Human sec
5	2211	100.0	431	4	AAB95464	Aab95464 Human pro
6	2211	100.0	431	4	AAB65299	Aab65299 Human PRO
7	2211	100.0	431	6	ABU55934	Abu55934 Human sec
8	2211	100.0	431	6	ABU58114	Abu58114 Human PRO
9	2211	100.0	431	6	ABU59192	Abu59192 Novel hum
10	2211	100.0	431	6	ABU82704	Abu82704 Human sec
11	2211	100.0	431	6	ABU60623	Abu60623 Human sec
12	2211	100.0	431	6	ABU14005	Abu14005 Human PRO
13	2211	100.0	431	6	ABU60244	Abu60244 Human PRO
14	2211	100.0	431	6	ABU72590	Abu72590 Novel hum
15	2211	100.0	431	6	ABU64930	Abu64930 Human sec
16	2211	100.0	431	6	ABU58364	Abu58364 Novel hum
17	2211	100.0	431	6	ABU57250	Abu57250 Human PRO
18	2211	100.0	431	6	ABU59339	Abu59339 Human sec
19	2211	100.0	431	6	ABO26036	Abo26036 Human PRO
20	2211	100.0	431	6	ABU56315	Abu56315 Human sec
21	2211	100.0	431	6	ABU60355	Abu60355 Novel hum
22	2211	100.0	431	6	ABU59045	Abu59045 Human sec
23	2211	100.0	431	6	ABU92423	Abu92423 Novel hum
24	2211	100.0	431	6	ABU59488	Abu59488 Novel hum
25	2211	100.0	431	6	ABU92254	Abu92254 Novel hum
26	2211	100.0	431	6	ABU10960	Abu10960 Human PRO
27	2211	100.0	431	6	ABU11316	Abu11316 Human pro
28	2211	100.0	431	6	ABU67135	Abu67135 Human PRO
29	2211	100.0	431	6	ABU81712	Abu81712 Novel hum
30	2211	100.0	431	6	ABU88651	Abu88651 Human sec
31	2211	100.0	431	6	ABO34165	Abo34165 Human PRO
32	2211	100.0	431	6	ADA38026	Ada38026 Human sec
33	2211	100.0	431	6	ADA21712	Ada21712 Human sec
34	2211	100.0	431	6	ADA10499	Ada10499 Human sec
35	2211	100.0	431	6	ADA18043	Ada18043 Human PRO
36	2211	100.0	431	6	ADA28151	Ada28151 Human sec
37	2211	100.0	431	6	ADA94731	Ada94731 Human sec
38	2211	100.0	431	6	ADA38956	Ada38956 Human sec
39	2211	100.0	431	6	ADA93077	Ada93077 Human sec
40	2211	100.0	431	7	ABO53251	Abo53251 Human sec
41	2211	100.0	431	7	ADA22638	Ada22638 Human sec
42	2211	100.0	431	7	ABO22621	Abo22621 Human sec
43	2211	100.0	431	7	ADA06804	Ada06804 Human sec
44	2211	100.0	431	7	ADA39497	Ada39497 Human sec
45	2211	100.0	431	7	ADB96523	Adb96523 Human PRO

ALIGNMENTS

RESULT 1
AAY17834
ID AAY17834 standard; protein; 431 AA.
XX
AC AAY17834;
XX
DT 12-AUG-1999 (first entry)
XX
DE Human PRO361 protein sequence.
XX
KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
KW secreted protein; transmembrane protein; inflammation disorder.
XX
OS Homo sapiens.
XX
PN WO9928462-A2.
XX
PD 10-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US025108.
XX
PR 03-DEC-1997; 97US-0067411P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 16-DEC-1997; 97US-0069694P.
PR 16-DEC-1997; 97US-0069696P.
PR 16-DEC-1997; 97US-0069702P.
PR 17-DEC-1997; 97US-0069870P.
PR 17-DEC-1997; 97US-0069873P.
PR 18-DEC-1997; 97US-0068017P.
PR 05-JAN-1998; 98US-0070440P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-FEB-1998; 98US-0075945P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney AL, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-371118/31.
DR N-PSDB; AAX80059.
XX
PT Nucleic acids encoding PRO secreted and transmembrane proteins.
XX
PS Claim 12; Fig 37; 123pp; English.
XX

CC The present invention describes nucleic acids encoding PRO secreted and
CC transmembrane proteins used therapeutically. The PRO proteins have
CC cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
CC activity. The proteins and polynucleotides can be used in therapy,
CC identification of homologues, raising antibodies and design of probes and
CC primers. They can be used in a range of diseases related to proteins that
CC they have homology with, e.g. a PRO protein having homology to complement
CC proteins may be used in inflammatory responses
XX
SQ Sequence 431 AA;

Query Match 100.0%; Score 2211; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 4.9e-173;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
              ||||||||||| 
Db        421 DYLINGIYVDI 431
```

RESULT 2
AAB33428
ID AAB33428 standard; protein; 431 AA.
XX
AC AAB33428;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO361 protein UNQ316 SEQ ID NO:72.
XX
KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX
OS Homo sapiens.
XX
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US005841.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0125775P.
PR 12-APR-1999; 99US-0128849P.
PR 20-APR-1999; 99WO-US008615.
PR 28-APR-1999; 99US-0131445P.
PR 04-MAY-1999; 99US-0132371P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX
DR WPI; 2000-572271/53.
DR N-PSDB; AAC58593.
XX
PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
PS Claim 33; Fig 30; 309pp; English.
XX
CC The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and

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CC   peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC   disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC   or immune-mediated skin diseases, allergic diseases, immunological
CC   diseases of the lung, and transplantation associated diseases including
CC   graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC   represent PCR primers and hybridisation probes used in the isolation of
CC   human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC   represent human PRO polynucleotide and protein sequences given in the
CC   exemplification of the present invention
XX
SQ   Sequence 431 AA;

  Query Match             100.0%;  Score 2211;  DB 3;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-173;
  Matches  431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
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Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
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Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
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Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
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Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
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Db        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
              ||||||||||| 
Db        421 DYLINGIYVDI 431


RESULT 3
AAB01325
ID   AAB01325 standard; protein; 431 AA.
XX
AC   AAB01325;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Human PRO361 polypeptide.
XX
KW   PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243;
KW   PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347; PRO355; PRO353;
KW   PRO361; PRO365; transmembrane polypeptide; antibody; screening;
KW   detection; inhibition; probe; primer; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /label= Signal peptide
FT   Modified-site   4. .10
FT                   /note= "N-myristoylation site"
FT   Modified-site   48. .54
FT                   /note= "N-myristoylation site"
FT   Modified-site   50. .57
FT                   /note= "Tyrosine kinase phosphorylation site"
FT   Modified-site   72. .76
FT                   /note= "N-glycosylation site"
FT   Modified-site   222. .226
FT                   /note= "N-glycosylation site"
FT   Modified-site   251. .255
FT                   /note= "N-glycosylation site"
FT   Modified-site   315. .321
FT                   /note= "N-myristoylation site"
FT   Modified-site   327. .331
FT                   /note= "N-glycosylation site"
FT   Modified-site   352. .356
FT                   /note= "N-glycosylation site"
FT   Domain          384. .405
FT                   /label= Transmembrane domain
FT   Modified-site   415. .419
FT                   /note= "cAMP- and cGMP-dependent protein kinase
FT                   phosphorylation site"
XX
PN   WO200032776-A2.
XX
PD   08-JUN-2000.
XX
PF   01-DEC-1999;   99WO-US028301.
XX
PR   01-DEC-1998;   98WO-US025108.
PR   16-DEC-1998;   98US-0112850P.
PR   22-DEC-1998;   98US-0113296P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Botstein D,  Eaton DL,  Ferrara N,  Filvaroff E;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Grimaldi CJ,  Gurney AL;
PI   Hillan KJ,  Kljavin IJ,  Napier MA,  Roy MA,  Tumas D,  Wood WI;
XX
DR   WPI; 2000-412324/35.
DR   N-PSDB; AAA49567.
XX
PT   New human nucleic acids encoding secreted and transmembrane polypeptides,
PT   designated as PRO polypeptides, useful as pharmaceutical and diagnostic
PT   agents.
XX
PS   Claim 12; Fig 32; 187pp; English.
XX
CC   New human nucleic acids encoding secreted and transmembrane polypeptides
CC   which are designated as PRO polypeptides are described The membrane-bound
CC   proteins have various industrial applications, including as
CC   pharmaceutical and diagnostic agents. The membrane-bound proteins can
CC   also be employed for screening of potential peptide or small molecule
CC   inhibitors of the relevant receptor/ligand interaction. Anti-PRO
CC   antibodies are useful for the affinity purification of PRO from
CC   recombinant cell culture or natural sources
XX
SQ   Sequence 431 AA;

  Query Match             100.0%;  Score 2211;  DB 3;  Length 431;.
  Best Local Similarity   100.0%;  Pred. No. 4.9e-173;
  Matches  431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
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Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
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Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
                ||||||||||||
Db        421 DYLINGIYVDI 431
```

RESULT 4
AAB34739
ID AAB34739 standard; protein; 431 AA.
XX
AC AAB34739;
XX
DT 26-JAN-2001 (first entry)
XX
DE Human secreted protein encoded by DNA clone vo27 1.
XX
KW Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;
KW systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke;
KW haematopoiesis regulation; tissue regrowth; wound healing; haemophilia;
KW Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;
KW contraceptive; infection; growth inhibition; hyperproliferative disorder;
KW psoriasis.
XX
OS Homo sapiens.
XX
PN WO200055375-A1.
XX
PD 21-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-US007285.
XX
PR 17-MAR-1999; 99US-0124808P.
PR 17-MAR-1999; 99US-0124916P.
PR 17-AUG-1999; 99US-0149639P.
PR 01-OCT-1999; 99US-0157247P.
PR 29-NOV-1999; 99US-0167824P.
PR 15-FEB-2000; 2000US-0182711P.
XX
PA (ALPH-) ALPHAGENE INC.
XX
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-638211/61.
DR N-PSDB; AAC59840.
XX
PT Novel proteins and polypeptides useful for the treatment of e.g multiple
PT sclerosis, systemic lupus erythmatosus, rheumatoid arthritis, cancer,
PT Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers.
XX
PS Claim 114; Page 453-455; 493pp; English.
XX
CC This invention relates to 59 human secreted proteins and the nucleotide
CC sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745
CC represent the proteins and their encoding nucleotide sequences, and
CC sequences AAB34746-B34771 represent fragments of the proteins. Probes for
CC the DNA sequences are represented by sequences AAC59847-C59596. The
CC proteins exhibit neuroprotective, dermatological, immunosuppressive,
CC antiinflammatory, antianaemic, nootropic, antiparkinsonian,
CC cerebroprotective, haemostatic, vulnerary, cytostatic, antipsoriatic,
CC antibacterial, virucide, and fungicide activity. The proteins and
CC nucleotide sequences are useful as nutritional sources or supplements and
CC in research. The proteins are useful for treating immune deficiency and
CC disorders, which may be genetic or resulting from infections, autoimmune
CC disorders such as multiple sclerosis, systemic lupus erythmatosus,
CC rheumatoid arthritis, and for treating myeloid or lymphoid cell
CC deficiencies such as anaemias by regulating haematopoiesis. The proteins
CC are also useful in compositions for bone, cartilage, tendon, ligament
CC and/or nerve tissue growth or regeneration, for wound healing, tissue
CC repair and replacement and in the treatment of wounds, incisions and
CC ulcers. Other uses include in the treatment of central and peripheral
CC nervous system and neuropathies such as Alzheimer's and Parkinson's
CC diseases and Shy-Drager syndrome, and mechanical and traumatic disorders,
CC such as spinal cord disorders, head trauma and stroke. The proteins may
CC also be used as a contraceptive, and for treating coagulation disorders
CC such as haemophilias. The protein and nucleotide sequences with cadherin
CC activity are useful for treating cancer. Other uses for the protein
CC include for inhibiting the growth, infection or function of, or killing,
CC infectious agents such as bacteria, virus, fungi and other parasites, for
CC effecting bodily characteristics such as height, weight, hair colour,
CC effecting biorhythms or cardiac cycles or rhythms, effecting metabolism,
CC catabolism, anabolism, processing, utilization, storage or elimination of
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors,
CC effecting behavioural characteristics, providing analgesic effects and
CC for treating hyperproliferative disorders such as psoriasis
XX
SQ Sequence 431 AA;

Query Match 100.0%; Score 2211; DB 3; Length 431;
Best Local Similarity 100.0%; Pred. No. 4.9e-173;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
              ||||||||||||
Db        421 DYLINGIYVDI 431
```

RESULT 5
AAB95464
ID AAB95464 standard; protein; 431 AA.
XX
AC AAB95464;
XX
DT 26-JUN-2001 (first entry)
XX

DE Human protein sequence SEQ ID NO:17950.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 17950; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesising 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 431 AA;

Query Match 100.0%; Score 2211; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 4.9e-173;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
              ||||||||||||
Db        421 DYLINGIYVDI 431
```

RESULT 6
AAB65299
ID AAB65299 standard; protein; 431 AA.
XX
AC AAB65299;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO361 protein sequence SEQ ID NO:515.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;

```
PI   Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM,  Wood WI;
PI   Zhang Z;
XX
DR   WPI; 2001-032160/04.
DR   N-PSDB; AAF44268.
XX
PT   PRO polynucleotides used to produce polypeptides used to target bioactive
PT   molecules such as toxins, radiolabels or antibodies, to specific cells,
PT   to cause targeted cell death.
XX
PS   Claim 12; Fig 328; 935pp; English.
XX
CC   The present invention describes human secreted and transmembrane PRO
CC   proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC   be used for targeted delivery of bioactive molecules, such as toxins,
CC   radiolabels or antibodies, that cause cell death. PRO nucleotide
CC   sequences, and their fragments, can be used as hybridisation probes, in
CC   chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC   DNA. They may also be used to produce transgenic animals which are used
CC   to develop and screen therapeutically useful reagents. The PRO nucleotide
CC   and protein sequence can be used for tissue typing and in treating
CC   cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC   AAF44470 represent PCR primers and hybridisation probes used in the
CC   isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC   AAB65300 represent human PRO polynucleotide and protein sequences given
CC   in the exemplification of the present invention
XX
SQ   Sequence 431 AA;

  Query Match             100.0%;  Score 2211;  DB 4;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-173;
  Matches  431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
              ||||||||||| 
Db        421 DYLINGIYVDI 431


RESULT 7
ABU55934
ID   ABU55934 standard; protein; 431 AA.
XX
AC   ABU55934;
XX
DT   26-MAR-2003  (first entry)

XX
DE   Human secreted/transmembrane protein PRO361.
XX
KW   Human; PRO; secreted protein; transmembrane protein; anti-HIV;
KW   cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic;
KW   cardiant; AIDS; acquired immunodeficiency syndrome; cancer;
KW   atherosclerosis; inflammatory disease; diabetic complication;
KW   cardiac injury; organ failure.
XX
OS   Homo sapiens.
XX
PN   US2002142959-A1.
XX
PD   03-OCT-2002.
XX
PF   31-AUG-2001; 2001US-00944654.
XX
PR   16-SEP-1998;   98WO-US019330.
PR   01-DEC-1998;   98WO-US025108.
PR   22-JUN-1999;   99WO-US012252.
PR   15-SEP-1999;   99WO-US021090.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   16-DEC-1999;   99WO-US030095.
PR   11-FEB-2000; 2000WO-US003565.
PR   22-FEB-2000; 2000WO-US004414.
PR   02-MAR-2000; 2000WO-US005841.
PR   30-MAR-2000; 2000WO-US008439.
PR   22-MAY-2000; 2000WO-US014042.
PR   28-JUL-2000; 2000WO-US020710.
PR   01-DEC-2000; 2000WO-US032678.
PR   28-FEB-2001; 2001WO-US006520.
PR   25-MAY-2001; 2001US-00866028.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Botstein D,  Eaton DL,  Ferrara N,  Filvaroff E;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL;
PI   Hillan KJ,  Kljavin IJ,  Napier MA,  Roy MA,  Tumas D,  Wood WI;
XX
DR   WPI; 2003-174141/17.
DR   N-PSDB; ABX75504.
XX
PT   New isolated PRO polypeptide and encoding nucleic acid, useful for the
PT   diagnosis and treatment of disorders associated with the PRO polypeptide,
PT   such as AIDS, cancer, atherosclerosis, inflammatory disease and diabetes.
XX
PS   Claim 12; Fig 32; 178pp; English.
XX
CC   The invention relates to an isolated PRO polypeptide (a secreted or
CC   transmembrane protein) comprising: (a) at least 80% sequence identity or
CC   positives when compared to any of 15 sequences, fully defined in the
CC   specification, lacking or with its associated signal peptide; or (b) at
CC   least 80% sequence identity to a sequence encoded by the full-length
CC   coding sequence of a DNA deposited in the American Type Culture
CC   Collection (ATCC). Also included are: (1) an isolated nucleic acid
CC   comprising: (a) at least 80% sequence identity to a nucleotide sequence
CC   that encodes a PRO protein; (b) at least 80% sequence identity to a
CC   nucleotide sequence or full-length coding sequence with any of 15 fully
CC   defined sequences of 957-3441 base pairs, given in the specification; or
CC   (c) at least 80% sequence identity to a full-length coding sequence of a
CC   DNA deposited under ATCC Accession No. 209526, 209508, 209524, 209528,
CC   209530, 209523, 209492, 209532, 209531, 209529, 209527, 209570, 209618,
CC   209621 or 209619; (2) a vector comprising the nucleic acid; (3) a host
CC   cell comprising the vector which, when cultured under conditions suitable
CC   for expression of the PRO polypeptide, produces the PRO protein; (4) a
CC   chimeric molecule comprising PRO fused to a heterologous amino acid
CC   sequence; and (5) an anti-PRO antibody. The methods and compositions of
CC   the present invention are useful for the diagnosis and treatment of
CC   disorders associated with the PRO polypeptide, such as AIDS (acquired
CC   immunodeficiency syndrome), cancer, atherosclerosis, inflammatory
CC   disease, diabetic complications, cardiac injury and organ failure. The
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CC   antibodies can also be used in the different screening, therapeutic and
CC   biological assays. The present sequence represents a PRO protein
XX
SQ   Sequence 431 AA;

  Query Match           100.0%;  Score 2211;  DB 6;  Length 431;
  Best Local Similarity  100.0%;  Pred. No. 4.9e-173;
  Matches  431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
              |||||||||||
Db        421 DYLINGIYVDI 431


RESULT 8
ABU58114
ID   ABU58114 standard; protein; 431 AA.
XX
AC   ABU58114;
XX
DT   14-APR-2003  (first entry)
XX
DE   Human PRO polypeptide #146.
XX
KW   Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW   horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW   antibody-dependent enzyme mediated prodrug therapy.
XX
OS   Homo sapiens.
XX
PN   US2003027163-A1.
XX
PD   06-FEB-2003.
XX
PF   15-NOV-2001; 2001US-00997666.
XX
PR   16-JUN-1997;   97US-0049787P.
PR   17-OCT-1997;   97US-0062250P.
PR   05-NOV-1997;   97WO-US020069.
PR   12-NOV-1997;   97US-0065186P.
PR   13-NOV-1997;   97US-0065311P.
PR   24-NOV-1997;   97US-0066770P.
PR   25-FEB-1998;   98US-0075945P.
PR   20-MAR-1998;   98US-0078910P.
PR   28-APR-1998;   98US-0083322P.
PR   07-MAY-1998;   98US-0084600P.
PR   28-MAY-1998;   98US-0087106P.
PR   02-JUN-1998;   98US-0087607P.
PR   02-JUN-1998;   98US-0087609P.
PR   02-JUN-1998;   98US-0087759P.
PR   03-JUN-1998;   98US-0087827P.
PR   04-JUN-1998;   98US-0088021P.
PR   04-JUN-1998;   98US-0088025P.
PR   04-JUN-1998;   98US-0088026P.
PR   04-JUN-1998;   98US-0088028P.
PR   04-JUN-1998;   98US-0088029P.
PR   04-JUN-1998;   98US-0088030P.
PR   04-JUN-1998;   98US-0088033P.
PR   04-JUN-1998;   98US-0088326P.
PR   05-JUN-1998;   98US-0088167P.
PR   05-JUN-1998;   98US-0088202P.
PR   05-JUN-1998;   98US-0088212P.
PR   05-JUN-1998;   98US-0088217P.
PR   09-JUN-1998;   98US-0088655P.
PR   10-JUN-1998;   98US-0088734P.
PR   10-JUN-1998;   98US-0088738P.
PR   10-JUN-1998;   98US-0088742P.
PR   10-JUN-1998;   98US-0088810P.
PR   10-JUN-1998;   98US-0088824P.
PR   10-JUN-1998;   98US-0088826P.
PR   11-JUN-1998;   98US-0088858P.
PR   11-JUN-1998;   98US-0088861P.
PR   11-JUN-1998;   98US-0088876P.
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Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
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Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
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Db        421 DYLINGIYVDI 431


RESULT 9
ABU59192
ID   ABU59192 standard; protein; 431 AA.
XX
AC   ABU59192;
XX
DT   28-APR-2003  (first entry)
XX
DE   Novel human secreted or transmembrane protein PRO361.
XX
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KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosum; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2002132252-A1.
XX
PD 19-SEP-2002.
XX
PF 14-NOV-2001; 2001US-00990442.
XX
PR 16-JUN-1997; 97US-0049787P.
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PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
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PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
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PR 28-FEB-2001; 2001WO-US006520.
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PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-247083/24.
DR N-PSDB; ABX80473.
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.
XX
PS Claim 12; Fig 328; 648pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,

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CC   PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC   stimulated T-lymphocytes and are therapeutically useful for enhancing
CC   immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC   retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC   rod photoreceptor cells) and therefore are useful for treating retinal
CC   disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC   and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC   and therefore are useful for treating kidney disorders associated with
CC   decreased mesangial cell function such as Berger disease or other
CC   nephropathies associated with dermatitis, herpetiformis or Crohn's
CC   disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC   proliferation and/or redifferentiation of chondrocytes in culture and are
CC   thus useful for treating sports injuries, and arthritis. This is the
CC   amino acid sequence of a novel human PRO protein
XX
SQ   Sequence 431 AA;

  Query Match             100.0%;  Score 2211;  DB 6;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-173;
  Matches  431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

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Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
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Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
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Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
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Db        421 DYLINGIYVDI 431


RESULT 10
ABU82704
ID   ABU82704 standard; protein; 431 AA.
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AC   ABU82704;
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DT   26-JUN-2003  (first entry)
XX
DE   Human secreted/transmembrane protein PRO361.
XX
KW   Human; PRO; secreted protein; transmembrane protein;
KW   cardiac insufficiency disorders; angiogenesis; wound healing;
KW   cancerous tumour; immune response; retinal disorder; sight loss;
KW   retinitis pigmentosum; age-related macular degeneration; AMD;
KW   kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis;
KW   Crohn's disease; sports injury; arthritis.
XX
OS   Homo sapiens.
XX
PN   US2003032023-A1.
XX
PD   13-FEB-2003.
XX
PF   14-NOV-2001; 2001US-00990711.
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PR 01-DEC-1999; 99WO-US028301.
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PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
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PR 24-FEB-2000; 2000WO-US004914.
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PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
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PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
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PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.

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Best Local Similarity 100.0%; Pred. No. 4.9e-173;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11
ABU60623
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DT 01-MAY-2003 (first entry)
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DE Human secreted/transmembrane protein, #182.
XX
KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
KW diagnostic; therapeutic; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002160384-A1.
XX
PD 31-OCT-2002.
XX
PF 14-NOV-2001; 2001US-00992598.
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PR 16-JUN-1997; 97US-0049787P.
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PR 05-NOV-1997; 97WO-US020069.
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PR 18-JUN-1998; 98US-0089907P.
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PR 17-SEP-1998; 98WO-US019437.
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PR 01-DEC-1998; 98WO-US025108.
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PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
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PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
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PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
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PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-288106/28.
DR N-PSDB; ABX90451.
XX
PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX
PS Claim 12; Fig 328; 650pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for

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CC   PRO, and in affinity purification of PRO from recombinant cell culture or
CC   natural sources. The sequences presented in ABU60478-ABU60624 are the PRO
CC   polynucleotides of the invention. Note: The sequence data for this patent
CC   is also available in electronic format from USPTO at
CC   seqdata.uspto.gov/sequence.html
XX
SQ   Sequence 431 AA;

  Query Match            100.0%;  Score 2211;  DB 6;  Length 431;
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Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
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Db        421 DYLINGIYVDI 431


RESULT 12
ABU14005
ID   ABU14005 standard; protein; 431 AA.
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AC   ABU14005;
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DT   26-FEB-2003  (first entry)
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DE   Human PRO361 polypeptide.
XX
KW   Human; PRO polypeptide; secreted protein; transmembrane protein;
KW   genetic disorder; antibacterial; immunosuppressive.
XX
OS   Homo sapiens.
XX
PN   US2002103125-A1.
XX
PD   01-AUG-2002.
XX
PF   20-NOV-2001; 2001US-00989731.
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PR   16-JUN-1997;   97US-0049787P.
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PR   16-JUN-1998;   98US-0089440P.
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PR   18-JUN-1998;   98US-0089907P.
PR   18-JUN-1998;   98US-0089908P.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   02-JUN-1999;   99WO-US012252.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   06-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   30-MAR-2000; 2000WO-US008439.
PR   15-MAY-2000; 2000WO-US013358.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
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PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   01-DEC-2000; 2000WO-US032678.
PR   28-FEB-2001; 2001WO-US006520.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   28-AUG-2001; 2001US-00941992.
XX
PA   (GETH ) GENENTECH LTD.
XX
PI   Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI   Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI   Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI   Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI   Zhang Z;
XX
DR   WPI; 2003-102117/09.
DR   N-PSDB; ABX64297.
XX
PT   Novel secreted and transmembrane polypeptide for modulating biological
PT   activity of cell expressing the polypeptide, identifying agonists or
PT   antagonists of polypeptide, and as molecular weight markers.
XX
PS   Claim 12; Fig 328; 649pp; English.
XX
CC   The present invention relates to the isolation of novel human PRO
CC   polypeptides, and the polynucleotide sequences encoding them. The PRO
CC   polypeptides are secreted and transmembrane proteins. The PRO
CC   polypeptides are useful for detecting other PRO polypeptides, for linking
CC   bioactive molecules to cells expressing PRO polypeptides, for modulating
CC   biological activities of cells expressing PRO polypeptides, and for for
CC   identifying agonists or antagonists. The polynucleotide sequences
CC   encoding PRO polypeptides are useful as hybridisation probes, in
CC   chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC   in the preparation of PRO polypeptides, for generating transgenic animals
CC   or knockout animals, to construct hybridisation probes for mapping the
CC   gene which encodes the PRO polypeptide, and for the genetic analysis of
CC   individuals with genetic disorders, in gene therapy, for chromosome
CC   identification, as chromosome markers, and for generating probes for PCR,
CC   Northern analysis, Southern analysis and Western analysis. ABU13860-
CC   ABU14006 represent the human PRO polypeptides of the invention. Note: The
CC   sequence data for this patent was obtained in electronic format directly
CC   from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 431 AA;

  Query Match             100.0%;  Score 2211;  DB 6;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-173;
  Matches  431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
              ||||||||||| 
Db        421 DYLINGIYVDI 431


RESULT 13
ABU60244
ID   ABU60244 standard; protein; 431 AA.
XX
AC   ABU60244;
XX
DT   24-APR-2003  (first entry)
XX
DE   Human PRO polypeptide #15.
XX
KW   Human; PRO; secreted polypeptide; transmembrane polypeptide; cancer;
KW   inflammatory disease; atherosclerosis; cardiac injury; AIDS; infertility;
KW   birth defect; premature aging; diabetes; dog; cat; horse;
KW   acquired immunodeficiency syndrome; cow; sheep; pig; goat; rabbit;
KW   industry; cytostatic; antiinflammatory; cardiant; antiinfertility;
KW   anti-HIV; antiarteriosclerotic; antidiabetic.
XX
OS   Homo sapiens.
XX
PN   US2002132768-A1.
XX
PD   19-SEP-2002.
XX
PF   31-AUG-2001; 2001US-00945015.
XX
PR   03-DEC-1997;   97US-0067411P.
PR   11-DEC-1997;   97US-0069278P.
PR   11-DEC-1997;   97US-0069334P.
PR   11-DEC-1997;   97US-0069335P.
PR   12-DEC-1997;   97US-0069425P.
PR   16-DEC-1997;   97US-0069694P.
PR   16-DEC-1997;   97US-0069696P.
PR   16-DEC-1997;   97US-0069702P.
PR   17-DEC-1997;   97US-0069870P.
PR   17-DEC-1997;   97US-0069873P.
PR   18-DEC-1997;   97US-0068017P.
PR   05-JAN-1998;   98US-0070440P.
PR   09-FEB-1998;   98US-0074086P.
PR   09-FEB-1998;   98US-0074092P.
PR   25-FEB-1998;   98US-0075945P.
PR   16-SEP-1998;   98WO-US019330.
PR   01-DEC-1998;   98WO-US025108.
PR   16-DEC-1998;   98US-00216021.
PR   16-DEC-1998;   98US-0112850P.
PR   22-DEC-1998;   98US-00218517.
PR   22-DEC-1998;   98US-0113296P.
PR   03-MAR-1999;   99US-00254311.
PR   22-JUN-1999;   99WO-US012252.
PR   28-JUL-1999;   99US-0146222P.
PR   15-SEP-1999;   99WO-US021090.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   16-DEC-1999;   99WO-US030095.
PR   11-FEB-2000; 2000WO-US003565.
PR   22-FEB-2000; 2000WO-US004414.
PR   02-MAR-2000; 2000WO-US005841.
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PR   30-MAR-2000; 2000WO-US008439.
PR   22-MAY-2000; 2000WO-US014042.
PR   28-JUL-2000; 2000WO-US020710.
PR   01-DEC-2000; 2000WO-US032678.
PR   28-FEB-2001; 2001WO-US006520.
PR   25-MAY-2001; 2001US-00866028.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Botstein D,  Eaton DL,  Ferrara N,  Filvaroff E;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL;
PI   Hillan KJ,  Kljavin IJ,  Napier MA,  Roy MA,  Tumas D,  Wood WI;
XX
DR   WPI; 2003-174088/17.
DR   N-PSDB; ABX89495.
XX
PT   New secreted and transmembrane polypeptides (e.g. PRO241, for use in
PT   pharmaceuticals, diagnostics or bioreactors, particularly for detecting
PT   or treating e.g. cancers, infertility or acquired immunodeficiency
PT   syndrome in mammals.
XX
PS   Claim 1; Fig 32; 173pp; English.
XX
CC   The invention relates to a human secreted and transmembrane polypeptide
CC   (PRO) and the polynucleotide encoding it. The PRO polypeptide or
CC   polynucleotide is useful in pharmaceuticals, diagnostics, biosensors or
CC   bioreactors. These are particularly useful for detecting or treating
CC   cancers, inflammatory diseases, atherosclerosis, cardiac injury,
CC   infertility, birth defects, premature aging, acquired immunodeficiency
CC   syndrome (AIDS) and diabetic complications in mammals, e.g. humans, dogs,
CC   cats, cattle, horses, sheep, pigs, goats or rabbits. The sequences are
CC   also useful in biotechnological and medical research and in various
CC   industrial applications. Sequences ABU60230-ABU60245 represent human PRO
CC   polypeptides of the invention
XX
SQ   Sequence 431 AA;

  Query Match             100.0%;  Score 2211;  DB 6;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-173;
  Matches  431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
              |||||||||||
Db        421 DYLINGIYVDI 431
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RESULT 14
ABU72590
ID   ABU72590 standard; protein; 431 AA.
XX
AC   ABU72590;
XX
DT   17-JUN-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO361.
XX
KW   Human; secreted and transmembrane protein; cytostatic; anti-HIV;
KW   virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
KW   PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
KW   cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;
KW   lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
KW   drug screening.
XX
OS   Homo sapiens.
XX
PN   US2003003531-A1.
XX
PD   02-JAN-2003.
XX
PF   19-NOV-2001; 2001US-00989734.
XX
PR   16-JUN-1997;   97US-0049787P.
PR   17-OCT-1997;   97US-0062250P.
PR   05-NOV-1997;   97WO-US020069.
PR   12-NOV-1997;   97US-0065186P.
PR   13-NOV-1997;   97US-0065311P.
PR   24-NOV-1997;   97US-0066770P.
PR   25-FEB-1998;   98US-0075945P.
PR   20-MAR-1998;   98US-0078910P.
PR   28-APR-1998;   98US-0083322P.
PR   07-MAY-1998;   98US-0084600P.
PR   28-MAY-1998;   98US-0087106P.
PR   02-JUN-1998;   98US-0087607P.
PR   02-JUN-1998;   98US-0087609P.
PR   02-JUN-1998;   98US-0087759P.
PR   03-JUN-1998;   98US-0087827P.
PR   04-JUN-1998;   98US-0088021P.
PR   04-JUN-1998;   98US-0088025P.
PR   04-JUN-1998;   98US-0088026P.
PR   04-JUN-1998;   98US-0088028P.
PR   04-JUN-1998;   98US-0088029P.
PR   04-JUN-1998;   98US-0088030P.
PR   04-JUN-1998;   98US-0088033P.
PR   04-JUN-1998;   98US-0088326P.
PR   05-JUN-1998;   98US-0088167P.
PR   05-JUN-1998;   98US-0088202P.
PR   05-JUN-1998;   98US-0088212P.
PR   05-JUN-1998;   98US-0088217P.
PR   09-JUN-1998;   98US-0088655P.
PR   10-JUN-1998;   98US-0088734P.
PR   10-JUN-1998;   98US-0088738P.
PR   10-JUN-1998;   98US-0088742P.
PR   10-JUN-1998;   98US-0088810P.
PR   10-JUN-1998;   98US-0088824P.
PR   10-JUN-1998;   98US-0088826P.
PR   11-JUN-1998;   98US-0088858P.
PR   11-JUN-1998;   98US-0088861P.
PR   11-JUN-1998;   98US-0088876P.
PR   12-JUN-1998;   98US-0089105P.
PR   16-JUN-1998;   98US-0089440P.
PR   16-JUN-1998;   98US-0089512P.
PR   16-JUN-1998;   98US-0089514P.
PR   17-JUN-1998;   98US-0089532P.
PR   17-JUN-1998;   98US-0089538P.
PR   17-JUN-1998;   98US-0089598P.
PR   17-JUN-1998;   98US-0089599P.
PR   17-JUN-1998;   98US-0089600P.
PR   17-JUN-1998;   98US-0089653P.
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PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-352829/33.
DR N-PSDB; ACA64519.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
PT disease.
XX
PS Claim 12; Fig 328; 663pp; English.
XX
CC The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
CC are particularly useful for detecting or treating e.g. malignancies or
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
CC disease in mammals. The PRO polypeptides are useful in drug screening,
CC particularly as targets for therapeutic intervention in these diseases,
CC and in the diagnostic determination of the presence of these diseases.
CC The PRO polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This is the amino acid sequence of a novel
CC human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 431 AA;

Query Match 100.0%; Score 2211; DB 6; Length 431;
Best Local Similarity 100.0%; Pred. No. 4.9e-173;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
              |||||||||||
Db        421 DYLINGIYVDI 431
```

RESULT 15
ABU64930
ID ABU64930 standard; protein; 431 AA.
XX
AC ABU64930;
XX
DT 15-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO361.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW Cornelia de Lange syndrome; gene therapy; immune disorder;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defect; premature aging; cardiac injury; AIDS; cancer;
KW diabetic complication.
XX
OS Homo sapiens.
XX
PN US2002173463-A1.
XX
PD 21-NOV-2002.
XX
PF 31-AUG-2001; 2001US-00944944.

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XX
PR   03-DEC-1997;   97US-0067411P.
PR   11-DEC-1997;   97US-0069278P.
PR   11-DEC-1997;   97US-0069334P.
PR   11-DEC-1997;   97US-0069335P.
PR   12-DEC-1997;   97US-0069425P.
PR   16-DEC-1997;   97US-0069694P.
PR   16-DEC-1997;   97US-0069696P.
PR   16-DEC-1997;   97US-0069702P.
PR   17-DEC-1997;   97US-0069870P.
PR   17-DEC-1997;   97US-0069873P.
PR   18-DEC-1997;   97US-0068017P.
PR   05-JAN-1998;   98US-0070440P.
PR   09-FEB-1998;   98US-0074086P.
PR   09-FEB-1998;   98US-0074092P.
PR   25-FEB-1998;   98US-0075945P.
PR   16-SEP-1998;   98WO-US019330.
PR   01-DEC-1998;   98WO-US025108.
PR   16-DEC-1998;   98US-0112850P.
PR   22-DEC-1998;   98US-0113296P.
PR   02-JUN-1999;   99WO-US012252.
PR   28-JUL-1999;   99US-0146222P.
PR   15-SEP-1999;   99WO-US021090.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   16-DEC-1999;   99WO-US030095.
PR   11-FEB-2000; 2000WO-US003565.
PR   22-FEB-2000; 2000WO-US004414.
PR   02-MAR-2000; 2000WO-US005841.
PR   30-MAR-2000; 2000WO-US008439.
PR   22-MAY-2000; 2000WO-US014042.
PR   28-JUL-2000; 2000WO-US020710.
PR   01-DEC-2000; 2000WO-US032678.
PR   28-FEB-2001; 2001WO-US006520.
PR   25-MAY-2001; 2001US-00866028.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Botstein D,  Eaton DL,  Ferrara N,  Filvaroff E;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL;
PI   Hillan KJ,  Kljavin IJ,  Napier MA,  Roy MA,  Tumas D,  Wood WI;
XX
DR   WPI; 2003-311003/30.
DR   N-PSDB; ABX96832.
XX
PT   New transmembrane polypeptides and polynucleotides useful for chromosome
PT   identification, tissue typing, gene therapy, in chromosome and gene
PT   mapping, or as molecular weight markers.
XX
PS   Claim 12; Fig 32; 172pp; English.
XX
CC   The invention relates to an isolated nucleic acid encoding a secreted/
CC   transmembrane polypeptide (designated as PRO proteins). 15 PRO
CC   polypeptides and their encoding polynucleotides are disclosed. Also
CC   included are a vector comprising the PRO nucleic acid, a host cell
CC   comprising the vector, a process for producing a PRO polypeptide (by
CC   culturing the host cell under conditions for the expression of the PRO
CC   polypeptide, and recovering the PRO polypeptide from the cell culture, an
CC   isolated polypeptide having at least 80% amino acid sequence identity to
CC   the PRO polypeptides, a chimaeric molecule comprising PRO fused to a
CC   heterologous amino acid sequence and an antibody which specifically binds
CC   to PRO. The PRO nucleotide sequences are useful as hybridisation probes,
CC   in chromosome and gene mapping, in generating sense and antisense RNA or
CC   DNA, in generating transgenic or knock-out animals which can be used in
CC   the development and screening of therapeutically useful reagents, and in
CC   gene therapy. The polypeptides may be used as molecular weight markers
CC   for protein electrophoresis purposes. The PRO polypeptides and nucleic
CC   acids may also be used for chromosome identification, and tissue typing.
CC   PRO241 (identified as Chordin) is a candidate gene for Cornelia de Lange
CC   syndrome. Other PRO proteins are variously implicated in immune
CC   disorders, inflammatory disease, organ failure, atherosclerosis, cardiac
CC   injury, infertility, birth defects, premature aging, cardiac injury,
CC   AIDS, cancer and diabetic complications. The present sequence represents
CC   a PRO protein
XX
SQ   Sequence 431 AA;

  Query Match            100.0%;  Score 2211;  DB 6;  Length 431;
  Best Local Similarity  100.0%;  Pred. No. 4.9e-173;
  Matches  431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
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Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
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Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
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Db        421 DYLINGIYVDI 431


Search completed: April 26, 2005, 21:49:17
Job time : 129 secs
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OM protein - protein search, using sw model

Run on: April 26, 2005, 21:49:26 ; Search time 55 Seconds
(without alignments)
584.977 Million cell updates/sec

Title: US-10-735-014-83
Perfect score: 2211
Sequence: 1 MFFGGEGSLTYTLVIICFLT.....LRRKRYSRLDYLINGIYVDI 431

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2211	100.0	431	4	US-09-866-028-83	Sequence 83, Appl
2	2211	100.0	431	4	US-09-944-457-83	Sequence 83, Appl
3	183	8.3	266	4	US-09-489-847-332	Sequence 332, App
4	149.5	6.8	5179	4	US-09-538-092-1258	Sequence 1258, Ap
5	145.5	6.6	629	3	US-09-241-581B-6	Sequence 6, Appli
6	145.5	6.6	629	4	US-08-265-428-6	Sequence 6, Appli
7	145.5	6.6	629	5	PCT-US95-07721-6	Sequence 6, Appli
8	144.5	6.5	1140	4	US-09-538-092-647	Sequence 647, App
9	136	6.2	2870	4	US-09-479-467A-15	Sequence 15, Appl
10	136	6.2	3178	4	US-09-479-467A-4	Sequence 4, Appli
11	133	6.0	556	4	US-09-538-092-712	Sequence 712, App
12	132	6.0	788	4	US-09-294-663-3	Sequence 3, Appli
13	132	6.0	807	4	US-09-294-663-4	Sequence 4, Appli
14	129	5.8	175	3	US-08-700-651-12	Sequence 12, Appl
15	129	5.8	175	3	US-08-928-361B-17	Sequence 17, Appl
16	129	5.8	175	4	US-09-588-995A-17	Sequence 17, Appl
17	128	5.8	249	3	US-08-700-651-15	Sequence 15, Appl
18	128	5.8	249	3	US-08-928-361B-20	Sequence 20, Appl
19	128	5.8	249	4	US-09-588-995A-20	Sequence 20, Appl
20	128	5.8	870	4	US-09-538-092-77	Sequence 77, Appl
21	127.5	5.8	1601	4	US-09-345-473E-40	Sequence 40, Appl
22	127	5.7	288	4	US-09-216-393B-341	Sequence 341, App
23	127	5.7	288	4	US-09-216-393B-344	Sequence 344, App
24	127	5.7	357	1	US-08-078-683A-8	Sequence 8, Appli
25	127	5.7	357	4	US-08-471-970A-8	Sequence 8, Appli
26	127	5.7	357	4	US-09-723-677B-8	Sequence 8, Appli
27	126.5	5.7	1837	3	US-08-928-361B-5	Sequence 5, Appli
28	126.5	5.7	1837	4	US-09-588-995A-5	Sequence 5, Appli
29	126	5.7	878	4	US-09-556-706B-2	Sequence 2, Appli
30	126	5.7	878	4	US-09-724-418A-2	Sequence 2, Appli
31	125.5	5.7	1721	3	US-08-700-651-5	Sequence 5, Appli
32	125.5	5.7	1721	3	US-08-928-361B-6	Sequence 6, Appli
33	125.5	5.7	1721	4	US-09-588-995A-6	Sequence 6, Appli
34	125	5.7	2137	3	US-09-134-001C-4463	Sequence 4463, Ap
35	124.5	5.6	451	1	US-08-287-001A-2	Sequence 2, Appli
36	124.5	5.6	451	5	PCT-US95-09941-2	Sequence 2, Appli
37	124.5	5.6	1306	4	US-09-538-092-330	Sequence 330, App
38	124	5.6	827	4	US-09-248-796A-17307	Sequence 17307, A
39	123.5	5.6	638	4	US-09-248-796A-18750	Sequence 18750, A
40	123.5	5.6	806	1	US-08-270-076A-11	Sequence 11, Appl
41	123	5.6	150	3	US-08-928-361B-18	Sequence 18, Appl
42	123	5.6	150	4	US-09-588-995A-18	Sequence 18, Appl
43	123	5.6	216	3	US-08-928-361B-27	Sequence 27, Appl
44	123	5.6	334	4	US-09-197-970B-7	Sequence 7, Appli
45	122.5	5.5	542	4	US-09-538-092-289	Sequence 289, App

ALIGNMENTS

RESULT 1
US-09-866-028-83
; Sequence 83, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 83
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-83

Query Match 100.0%; Score 2211; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.9e-202;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
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Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
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Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
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Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
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Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
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Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

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Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
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Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
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Db        421 DYLINGIYVDI 431
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RESULT 2
US-09-944-457-83
; Sequence 83, Application US/09944457
; Patent No. 6734288
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: Decemberl, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 83
; LENGTH: 431
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; ORGANISM: Homo Sapien
US-09-944-457-83

Query Match 100.0%; Score 2211; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.9e-202;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
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Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
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Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
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Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
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Qy        421 DYLINGIYVDI 431
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Db        421 DYLINGIYVDI 431
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RESULT 3
US-09-489-847-332
; Sequence 332, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 332
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (195)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (199)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (206)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-489-847-332

Query Match 8.3%; Score 183; DB 4; Length 266;
Best Local Similarity 27.2%; Pred. No. 5e-09;
Matches 80; Conservative 42; Mismatches 116; Indels 56; Gaps 13;

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Qy        158 TDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAH 217
              |: :  ||:|   |     |::| :  :     ||:   |         :  :|   :|
Db          5 TEDTSRTDVSEPATSG---GAADGVTSIAPTAVASSTTAA-------SITTAASSMTVAS 54

Qy        218 LLPENVSALPATVAVASPHT-----TSATPKPATL-LPTNASV----TPS--GTSQPQLA 265
              |   :|   |||  :| |     |:|:  | || ||   |     |||   | | |:
Db         55 SAP-TTAASSTTVASIAPTTTASSMTAASSTPMTLALPAPTSTXTGRTPSTTATGHPSLS 113

Qy        266 TTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQA-PTDSKGSLETIPFTE 324
              |    |   :: | |  ::|: |||    | :||||  ::     |: ||       :
Db        114 TALAQVPKSSALPRTATLATLATRA----QTVATTANTSSPMSTRPSPSKHMPSDTAASP 169

Qy        325 ISNLTLNTGNVYNPTA---LSMSNVESSTMNKTASWEGREASPGSSSQGSVPENQYGLPF 381
              :  :        | |   :|  :|:   :| |                :| |    |
Db        170 VPPMX--------PQAQGPISQVSVDQPVVNTT-----------XKSTXMPSNTTXEPL 209

Qy        382 -----EKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVD 430
                  :| ||:  || ||   :  |||      || ::| |:::||||||:| |
Db        210 TQAVVDKTLLLVVLLLGVTLFITVLVLFALQAYESYKKKDYTQVDYLINGMYAD 263
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RESULT 4
US-09-538-092-1258
; Sequence 1258, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1258
; LENGTH: 5179
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q02817
US-09-538-092-1258

Query Match 6.8%; Score 149.5; DB 4; Length 5179;
Best Local Similarity 34.1%; Pred. No. 0.00095;
Matches 43; Conservative 12; Mismatches 52; Indels 19; Gaps 4;

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Qy        220 PENVSALPATVAVASPHTTSATPKPATL--LPTNASVTP--SGTSQPQLATTAPPVTTVT 275
              | : : || |   : | ||: || | |    ||   :||  | |: |   | :|| || |
Db       1511 PASTTTLPPTTTPSPPTTTTTTPPPTTTPSPPTTTPITPPTSTTTLPPTTTPSPPPTTTT 1570

Qy        276 SQPPTTLIS-----------TVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFT 323
              : ||||  |           |  |    | :  ||   |||   || :     | | |
Db       1571 TPPPTTTPSPPTTTTPSPPTITTTTPPPTTTPSPPTT---TTTTPPPTTTPSPPTTTPIT 1627

Qy        324 EISNLT 329
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Db       1628 PPTSTT 1633
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RESULT 5
US-09-241-581B-6
; Sequence 6, Application US/09241581B
; Patent No. 6350859
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology

; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/241,581B
; FILING DATE: 02-Feb-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 629 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..629
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; Drosophila Melanogaster Scavenger Receptor
; Class CI."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 30..353
; OTHER INFORMATION: /note= "Positions 30-32, 90-92,
; 129-131, 180-182, 253-255 and 351-353
; represent potential N-glycosylation
; sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..20
; OTHER INFORMATION: /note= "Amino acids 1-20 represent
; a putative signal sequence."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..74
; OTHER INFORMATION: /note= "Amino acids 21-74 represent
; complement control protein domain
; number 1."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 75..127
; OTHER INFORMATION: /note= "Amino acids 75-127
; represent complement control protein
; domain number 2."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 128..312
; OTHER INFORMATION: /note= "Amino acids 128-312
; represent an MAM domain."
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 22..381
; OTHER INFORMATION: /note= "The cysteines at positions
; 22, 45, 59, 72, 77, 99, 113, 125, 136, 144, 216,
; 217, 254, 310, 339, 343, 361, 363, 367, 373, 374
; and 381 represent potential disulfide linkages."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 338..381
; OTHER INFORMATION: /note= "Amino acids 338-381
; represent a somatomedin B domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 387..514
; OTHER INFORMATION: /note= "Amino acids 387-514
; represent a mucin-like potential
; O-linked glycosylation region."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 544..564
; OTHER INFORMATION: /note= "Amino acids 544-565
; represent a putative TM domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 565..629
; OTHER INFORMATION: /note= "Amino acids 565-629
; represent a putative cytoplasmic
; domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 576..602
; OTHER INFORMATION: /note= "Amino acids 576-579 and
; 599-602 represent casein kinase II
; sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 578..592
; OTHER INFORMATION: /note= "Amino acids 578-580 and
; 590-592 represent protein kinase C
; sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 596..599
; OTHER INFORMATION: /note= "Amino acids 596-599
; represent a cAMP protein kinase site."
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-241-581B-6

Query Match 6.6%; Score 145.5; DB 3; Length 629;
Best Local Similarity 22.9%; Pred. No. 7.6e-05;
Matches 48; Conservative 30; Mismatches 79; Indels 53; Gaps 5;

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Qy        213 QEIAHLLPENVSALPATVAVASPHT-----------TSATPKPATLLPTNASVTPSGTSQ 261
              :|:     :::|:|| ||   |  |           |: |    |  ||  : |   |:
Db        383 KELLTTTEDDISSLPPTVTSTSTSTTRKSTTTTTSTTTSTTTTKRPTTTTTTTKATTT 442

Qy        262 PQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIP 321
               :  ||  | || |:  |||  ||      :|    :||   |||    |  |
Db        443 KRTTTTKKPTTTSTTPKPTTTTSTTPKSTTSTTSTTSTTPTTTTTINVFTTKK------- 495

Qy        322 FTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASW-------EGREASPGSSSQGSVPE 374
                  : : : | :    | :    : :    |  :|       ||   : ||:   ::
Db        496 ----TTIMIPTSSTEKTTGI----ITTMKTRKRITWNVDPQDIEGHMDTSGSTPNPALV- 546

Qy        375 NQYGLPPEKWLLIGSLLFGVLFLVIGLVLL 404
                              ||:|::|:||:
Db        547 ------------------VLYLLLGIVLV 557
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RESULT 6
US-08-265-428-6
; Sequence 6, Application US/08265428
; Patent No. 6429289
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: Class BI Scavenger Receptors

```
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  1100 Peachtree Street, Suite 2800
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30309-4530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,428
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  MIT6620
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (404) 815-6508
;      TELEFAX:  (404) 815-6555
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  629 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  misc. feature
;      LOCATION:  1..629
;      OTHER INFORMATION:  /Function = "Amino acid sequence for the Drosophila Melanogas
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  30..353
;      OTHER INFORMATION:  /note= "Positions 30-32, 90-92,
;      OTHER INFORMATION:  129-131, 180-182, 253-255 and 351-353 represent
;      OTHER INFORMATION:  potential N-glycosylation sites."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1..20
;      OTHER INFORMATION:  /note= "Amino acids 1-20 represent
;      OTHER INFORMATION:  a putative signal sequence."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  21..74
;      OTHER INFORMATION:  /note= "Amino acids 21-74 represent
;      OTHER INFORMATION:  complement control protein domain number 1."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  75..127
;      OTHER INFORMATION:  /note= "Amino acids 75-127
;      OTHER INFORMATION:  represent complement control protein domain number
;      OTHER INFORMATION:  2."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  128..312
;      OTHER INFORMATION:  /note= "Amino acids 128-312
;      OTHER INFORMATION:  represent an MAM domain."
;    FEATURE:
;      NAME/KEY:  Disulfide-bond
;      LOCATION:  22..381
;      OTHER INFORMATION:  /note= "The cysteines at positions
;      OTHER INFORMATION:  22, 45, 59, 72, 77, 99, 113, 125, 136, 144, 216,
;      OTHER INFORMATION:  217, 254, 310, 339, 343, 361, 363, 367, 373, 374 and 381
;      OTHER INFORMATION:  represent potential disulfide linkages."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  338..381
;      OTHER INFORMATION:  /note= "Amino acids 338-381
;      OTHER INFORMATION:  represent a somatomedin B domain."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  387..514
;      OTHER INFORMATION:  /note= "Amino acids 387-514
;      OTHER INFORMATION:  represent a mucin-like potential O-linked
;      OTHER INFORMATION:  glycosylation region."
;    FEATURE:
;      NAME/KEY:  Domain
;      LOCATION:  544..564
;      OTHER INFORMATION:  /note= "Amino acids 544-565
;      OTHER INFORMATION:  represent a putative TM domain."
;    FEATURE:
;      NAME/KEY:  Domain
;      LOCATION:  565..629
;      OTHER INFORMATION:  /note= "Amino acids 565-629
;      OTHER INFORMATION:  represent a putative cytoplasmic domain."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  576..602
;      OTHER INFORMATION:  /note= "Amino acids 576-579 and
;      OTHER INFORMATION:  599-602 represent casein kinase II sites."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  578..592
;      OTHER INFORMATION:  /note= "Amino acids 578-580 and
;      OTHER INFORMATION:  590-592 represent protein kinase C sites."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  596..599
;      OTHER INFORMATION:  /note= "Amino acids 596-599
;      OTHER INFORMATION:  represent a cAMP protein kinase site."
US-08-265-428-6

  Query Match             6.6%;  Score 145.5;  DB 4;  Length 629;
  Best Local Similarity   22.9%;  Pred. No. 7.6e-05;
  Matches   48;  Conservative   30;  Mismatches   79;  Indels   53;  Gaps    5;

Qy        213 QEIAHLLPENVSALPATVAVASPHT----------TSATPKPATLLPTNASVTPSGTSQ 261
              :|:     :::|:|| ||   |  |           |: |    |  ||  : |   |:
Db        383 KELLTTTEDDISSLPPTVTSTSTSTTRKSTTTTTSTTTSTTTTKRPTTTTTTTKATTT 442

Qy        262 PQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIP 321
               :  ||  | || |:  |||  ||       :|    :||   |||    | |
Db        443 KRTTTTKKPTTTSTTPKPTTTTSTTPKSTTSTTSTTSTTPTTTTTINVFTTKK------- 495

Qy        322 FTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASW-------EGREASPGSSSQGSVPE 374
                  : : : | :    | :    : :    |  :|       ||   : ||:   ::
Db        496 ----TTIMIPTSSTEKTTGI----ITTMKTRKRITWNVDPQDIEGHMDTSGSTPNPALV- 546

Qy        375 NQYGLPFEKWLLIGSLLFGVLFLVIGLVLL 404
                                 ||:|::|:||:
Db        547 ------------------VLYLLLGIVLV 557


RESULT 7
PCT-US95-07721-6
; Sequence 6, Application PC/TUS9507721
;  GENERAL INFORMATION:
;    APPLICANT:  Massachusetts Institute of Technology
;    TITLE OF INVENTION:  Class BI and CI Scavenger Receptors
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  2800 One Atlantic Center
;      STREET:  1201 West Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30309-3450
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/07721
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  MIT6620
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (404) 873-8794
;      TELEFAX:  (404) 873-8795
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  629 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  misc. feature
;      LOCATION:  1..629
;      OTHER INFORMATION:  /Function = "Amino acid sequence for the
;      OTHER INFORMATION:  Drosophila Melanogaster Scavenger Receptor
;      OTHER INFORMATION:  Class CI."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  30..353
;      OTHER INFORMATION:  /note= "Positions 30-32, 90-92,
;      OTHER INFORMATION:  129-131, 180-182, 253-255 and 351-353
;      OTHER INFORMATION:  represent potential N-glycosylation
;      OTHER INFORMATION:  sites."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1..20
;      OTHER INFORMATION:  /note= "Amino acids 1-20 represent
;      OTHER INFORMATION:  a putative signal sequence."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  21..74
;      OTHER INFORMATION:  /note= "Amino acids 21-74 represent
;      OTHER INFORMATION:  complement control protein domain
;      OTHER INFORMATION:  number 1."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  75..127
;      OTHER INFORMATION:  /note= "Amino acids 75-127
;      OTHER INFORMATION:  represent complement control protein
;      OTHER INFORMATION:  domain number 2."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  128..312
;      OTHER INFORMATION:  /note= "Amino acids 128-312
;      OTHER INFORMATION:  represent an MAM domain."
;    FEATURE:
;      NAME/KEY:  Disulfide-bond
;      LOCATION:  22..381
;      OTHER INFORMATION:  /note= "The cysteines at positions
;      OTHER INFORMATION:  22, 45, 59, 72, 77, 99, 113, 125, 136, 144, 216,
;      OTHER INFORMATION:  217, 254, 310, 339, 343, 361, 363, 367, 373, 374
;      OTHER INFORMATION:  and 381 represent potential disulfide linkages."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  338..381
;      OTHER INFORMATION:  /note= "Amino acids 338-381
;      OTHER INFORMATION:  represent a somatomedin B domain."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  387..514
;      OTHER INFORMATION:  /note= "Amino acids 387-514
;      OTHER INFORMATION:  represent a mucin-like potential
;      OTHER INFORMATION:  O-linked glycosylation region."
;    FEATURE:
;      NAME/KEY:  Domain
;      LOCATION:  544..564
;      OTHER INFORMATION:  /note= "Amino acids 544-565
;      OTHER INFORMATION:  represent a putative TM domain."
;    FEATURE:
;      NAME/KEY:  Domain
;      LOCATION:  565..629
;      OTHER INFORMATION:  /note= "Amino acids 565-629
;      OTHER INFORMATION:  represent a putative cytoplasmic
;      OTHER INFORMATION:  domain."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  576..602
;      OTHER INFORMATION:  /note= "Amino acids 576-579 and
;      OTHER INFORMATION:  599-602 represent casein kinase II
;      OTHER INFORMATION:  sites."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  578..592
;      OTHER INFORMATION:  /note= "Amino acids 578-580 and
;      OTHER INFORMATION:  590-592 represent protein kinase C
;      OTHER INFORMATION:  sites."
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  596..599
;      OTHER INFORMATION:  /note= "Amino acids 596-599
;      OTHER INFORMATION:  represent a cAMP protein kinase site."
PCT-US95-07721-6

  Query Match             6.6%;  Score 145.5;  DB 5;  Length 629;
  Best Local Similarity   22.9%;  Pred. No. 7.6e-05;
  Matches   48;  Conservative   30;  Mismatches   79;  Indels   53;  Gaps    5;

Qy        213 QEIAHLLPENVSALPATVAVASPHT----------TSATPKPATLLPTNASVTPSGTSQ 261
              :|:     :::|:|| ||   |  |         |: |    |  ||  : |   |:
Db        383 KELLTTTEDDISSLPPTVTSTSTSTTRKSTTTTTSTTTTSTTTTKRPTTTTTTKATTT 442

Qy        262 PQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIP 321
                :  ||  | || |:  |||  ||      :|    :||   |||    |  |
Db        443 KRTTTTKKPTTTSTTPKPTTTTSTTPKSTTSTTSTTSTTPTTTTTINVFTTKK------- 495

Qy        322 FTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASW-------EGREASPGSSSQGSVPE 374
                : : : | :    | :   : :   |  :|       ||   : ||:   ::
Db        496 ----TTIMIPTSSTEKTTGI----ITTMKTRKRITWNVDPQDIEGHMDTSGSTPNPALV- 546

Qy        375 NQYGLPFEKWLLIGSLLFGVLFLVIGLVLL 404
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Db        547 -------------------VLYLLLGIVLV 557


RESULT 8
US-09-538-092-647
; Sequence 647, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 647
;   LENGTH: 1140
;   TYPE: PRT
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;   ORGANISM: Saccharomyces cerevisiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number YMR317W
US-09-538-092-647

  Query Match             6.5%;  Score 144.5;  DB 4;  Length 1140;
  Best Local Similarity   21.2%;  Pred. No. 0.00025;
  Matches   86;  Conservative   63;  Mismatches  169;  Indels   87;  Gaps   13;

Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVID--IQSSLSKGIRGNEPVYTS 58
              :|      |:| |||         |:  : |: | | :  :  |:|||| |        ||
Db        456 LFSSKNTSVTSTLV-----ATEASSVTSSLRPSSETLASNSIIESSLSTGYNSTVSTTTS 510

Qy         59 TQEDCINSCCSTKN----------ISGDKACNLMIFDTRKT-ARQPNCYLFFCPNEEACP 107
                : |  |: |           | | : : :||    |    |:  :       :
Db        511 AASSTLGSKVSSSNSRMATSKTSSTSSDLSKSSVIFGNSSTVTTSPSASI-------SLT 563

Qy        108 LKPAKGLMSYRIITDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDIS 167
                |   : |    ::  |:: || |   | :::      | ||      |  |  : |
Db        564 ASPLPSVWSDITSSEASSISSNLASSSAPSDNNSTIASASLIVT-----KTKNSVVSSIV 618

Qy        168 WRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQ----------FSSDQEI 215
                | |:    |:       :  :|  ||: |    | |:             |||
Db        619 SSITSSETTNESN-------LATSSTSLLSNKATARSLSTSNATSASNVPTGTFSSMSSH 671

Qy        216 AHLLPENVSALPATVAVASP----------HTTSATPKPATLLPTNASVTPSGTSQPQL 264
              ::    |   |::|: |           |  ::|  :||: : |  | |      :
Db        672 TSVITPGFSTSSASLAINSTVVSSSLAGYSFSTPESSPTTSTLVTSEAPSTVS-----SM 726

Qy        265 ATTAPPVTTVTSQPPTTLISTVFTRAAATLQAM---------ATTAVLTTTFQAPTDSKG 315
              |:|| :   ||  |:   ::  | : ::: ::         :  |   ||| ||: |
Db        727 TTSAPFINNSTSARPSPSTASFITESTSSISSVPLASGDVTSSLAAHNLTTFSAPSTSSA 786

Qy        316 SLETIPFTEISNLTLNTGNVYNP------TALSMSNVESSTMNKT 354
              |       :|  | ::  :  |       : : | : :|  |||
Db        787 QL-------VSKSTTSSSILVTPRIDRSGNSSTASRIATSLPNKT 824


RESULT 9
US-09-479-467A-15
; Sequence 15, Application US/09479467A
; Patent No. 6723557
; GENERAL INFORMATION:
;  APPLICANT:     Sternberg, Paul W.
;  APPLICANT:  Barr, Maureen M.
;  TITLE OF INVENTION:     POLYCYSTIC KIDNEY DISEASE GENE HOMOLOGS REQUIRED FOR MALE MAT
;  TITLE OF INVENTION:  BEHAVIOR IN NEMATODES AND ASSAYS BASED THEREON
;  FILE REFERENCE:     18021-2901B
;  CURRENT APPLICATION NUMBER: US/09/479,467A
;  CURRENT FILING DATE:  2000-01-06
;  PRIOR APPLICATION NUMBER:     60/115,127
;  PRIOR FILING DATE:     1999-01-06
;  NUMBER OF SEQ ID NOS:     16
;  SOFTWARE:     PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 2870
;   TYPE: PRT
;   ORGANISM: C. Elegans Lov-1 sy582 deletion protein
US-09-479-467A-15

  Query Match             6.2%;  Score 136;  DB 4;  Length 2870;
  Best Local Similarity   23.6%;  Pred. No. 0.0071;
  Matches   37;  Conservative   38;  Mismatches   70;  Indels   12;  Gaps    2;

Qy        221 ENVSALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPT 280
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Db        405 EEPSTSTTTTEVTSTSSTVTTTEPTTTLTTSTAST---------STTEPSTSTVTTSPST 455

Qy        281 TLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTA 340
              : :::  | ::::   : |     :|  :|: :  :  | | |  :  : ::    :  :
Db        456 SPVTSTVTSSSSSSTTVTTPTSTESTSTSPSSTVTTSTTAPSTSTTGPSSSSSTPSSTAS 515

Qy        341 LSMSNVESSTMNKTASWEG---REASPGSSSQGSVPE 374
              |:|:  ||| : |:: :     ::   :|| |: |:
Db        516 SSVSSTASSTQSSTSTQQSSTTTKSETTTSSDGTNPD 552


RESULT 10
US-09-479-467A-4
; Sequence 4, Application US/09479467A
; Patent No. 6723557
; GENERAL INFORMATION:
;  APPLICANT:     Sternberg, Paul W.
;  APPLICANT:  Barr, Maureen M.
;  TITLE OF INVENTION:     POLYCYSTIC KIDNEY DISEASE GENE HOMOLOGS REQUIRED FOR MALE MA
;  TITLE OF INVENTION:  BEHAVIOR IN NEMATODES AND ASSAYS BASED THEREON
;  FILE REFERENCE:     18021-2901B
;  CURRENT APPLICATION NUMBER: US/09/479,467A
;  CURRENT FILING DATE:  2000-01-06
;  PRIOR APPLICATION NUMBER:     60/115,127
;  PRIOR FILING DATE:     1999-01-06
;  NUMBER OF SEQ ID NOS:     16
;  SOFTWARE:     PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 3178
;   TYPE: PRT
;   ORGANISM: C. Elegans Lov-1 protein
US-09-479-467A-4

  Query Match             6.2%;  Score 136;  DB 4;  Length 3178;
  Best Local Similarity   23.6%;  Pred. No. 0.0084;
  Matches   37;  Conservative   38;  Mismatches   70;  Indels   12;  Gaps    2;

Qy        221 ENVSALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPT 280
              |  |     |  | |  :|  | :| | | |: : |         :|| |  :|||: | |
Db        405 EEPSTSTTTTEVTSTSSTVTTTEPTTTLTTSTAST---------STTEPSTSTVTTSPST 455

Qy        281 TLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTA 340
              : :::  | ::::   : |     :|  :|: :  :  | | |  :  : ::    :  :
Db        456 SPVTSTVTSSSSSSTTVTTPTSTESTSTSPSSTVTTSTTAPSTSTTGPSSSSSTPSSTAS 515

Qy        341 LSMSNVESSTMNKTASWEG---REASPGSSSQGSVPE 374
              |:|:  ||| : |:: :     ::   :|| |: |:
Db        516 SSVSSTASSTQSSTSTQQSSTTTKSETTTSSDGTNPD 552


RESULT 11
US-09-538-092-712
; Sequence 712, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 712
;   LENGTH: 556
;   TYPE: PRT
;   ORGANISM: Saccharomyces cerevisiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number YOL105C
US-09-538-092-712

  Query Match             6.0%;  Score 133;  DB 4;  Length 556;
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  Best Local Similarity   22.6%;  Pred. No. 0.00097;
  Matches   68;  Conservative   57;  Mismatches  114;  Indels   62;  Gaps   10;

Qy        164 TDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENV 223
              | :|  :: | | |||           :|||:        | : : |:| : : ::   |
Db        134 TFVSSVESSSSKEGSSTSYMPSTTSSLSSAQI-------SSTTRRTSTDMKSSEMIATTV 186

Qy        224 SALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLI 283
              |     | :  |  |:| |   :|   | :| | | ||    :||:   :: ||   ||
Db        187 STTSTTSSSTSSTTSSTT--SSTTSSTTSSTTSSSTSSTTSSTTSSTTSS--TTSS 242

Qy        284 STVFTRAAATLQAMATTAVLT--------------TTFQAPTDS--------KGSLETI 320
              :|  | :: |    :||:: :              ||  : | |          |  |:
Db        243 TTSSTTSSTT---SSTTSIFSVTSSSSSITLSSSEHTTVDSRTSSPSSTLVPVSSSSSTL 299

Qy        321 PFTEISNLTLNTG------------NVYNPTALSMSNVESSTMNKTASWEGREASPGSS 367
                :::::| :|              :|     :| |:    |: | :     :|  ::
Db        300 STPKVTSMTPSTSSTIPIVTSVELVTSVVTKAIVSTSDQHQETIFVTRTSVVERSSEVAT 359

Qy        368 SQGSVPENQYGLPFEKWLLIGSL-------LFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
              : :   |:     :: |  |::       :|||:|:  |:|| |     ||| : :|
Db        360 ATAAASNNRSNSTSKQRLSGGAIAGIVIGVVFGVIFII--LILLFLIWR---RRKSHDQL 414

Qy        421 D 421
              |
Db        415 D 415


RESULT 12
US-09-294-663-3
; Sequence 3, Application US/09294663
; Patent No. 6765127
;  GENERAL INFORMATION:
;    APPLICANT:  Granados, Robert R
;    APPLICANT:  Wang, Ping
;    TITLE OF INVENTION:  A No. 6765127el Invertebrate Intestinal Mucin
;    TITLE OF INVENTION:  cDNA and Related Products and Methods
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Pinnisi & Michaels, P.C.
;      STREET:  118 No. 6765127th Tioga Street
;      CITY:  Ithaca
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  14850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/294,663
;      FILING DATE:  19-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/103,429
;      FILING DATE:  24-JUN-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michaels, Christopher A
;      REGISTRATION NUMBER:  34,390
;      REFERENCE/DOCKET NUMBER:  BTI-39-CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (607) 256-2000
;      TELEFAX:  (607) 256-3628
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  788 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Trichoplusia ni
;      TISSUE TYPE:  peritrophic membrane
US-09-294-663-3

  Query Match             6.0%;  Score 132;  DB 4;  Length 788;
  Best Local Similarity   31.0%;  Pred. No. 0.0021;
  Matches   48;  Conservative   15;  Mismatches   78;  Indels   14;  Gaps    6;

Qy        220 PENVSALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPP 279
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Db         96 PAETTQAPAT--TQAPTTTQA-PTTTTQAPTTTTQAPTTTTQAPTTTQAP---TTTQAPT 149

Qy        280 TTLISTVFTRA-AATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNP 338
              ||    |  |:|    | ||  ||    || |||| ::    |   | |:    |    |
Db        150 TTQAPTTTTQAPTTTTQAPTTTTQAPTTTQAPTTTQAPTTTQAPTTITQ-AATTPAATTP 208

Qy        339 TALSMSNVESSTMNKTASWEGREASPGSSSQGSVP 373
                | : :    :     |:      :||  :  | |
Db        209 AATTPAATTPAATTPAAT------TPGVPAPTSAP 237


RESULT 13
US-09-294-663-4
; Sequence 4, Application US/09294663
; Patent No. 6765127
;  GENERAL INFORMATION:
;    APPLICANT:  Granados, Robert R
;    APPLICANT:  Wang, Ping
;    TITLE OF INVENTION:  A No. 6765127el Invertebrate Intestinal Mucin
;    TITLE OF INVENTION:  cDNA and Related Products and Methods
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Pinnisi & Michaels, P.C.
;      STREET:  118 No. 6765127th Tioga Street
;      CITY:  Ithaca
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  14850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/294,663
;      FILING DATE:  19-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/103,429
;      FILING DATE:  24-JUN-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michaels, Christopher A
;      REGISTRATION NUMBER:  34,390
;      REFERENCE/DOCKET NUMBER:  BTI-39-CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (607) 256-2000
;      TELEFAX:  (607) 256-3628
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  807 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Trichoplusia ni
;      TISSUE TYPE:  peritrophic membrane
US-09-294-663-4

  Query Match             6.0%;  Score 132;  DB 4;  Length 807;
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  Best Local Similarity   31.0%;  Pred. No. 0.0022;
  Matches   48;  Conservative   15;  Mismatches   78;  Indels   14;  Gaps    6;

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Db         96 PAETTQAPAT--TQAPTTTQA-PTTTTQAPTTTTQAPTTTTQAPTTTQAP---TTTQAPT 149

Qy        280 TTLISTVFTRA-AATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNP 338
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Db        150 TTQAPTTTTQAPTTTTQAPTTTTQAPTTTQAPTTTQAPTTTQAPTTITQ-AATTPAATTP 208

Qy        339 TALSMSNVESSTMNKTASWEGREASPGSSSQGSVP 373
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Db        209 AATTPAATTPAATTPAAT------TPGVPAPTSAP 237


RESULT 14
US-08-700-651-12
; Sequence 12, Application US/08700651B
; Patent No. 6015882
; GENERAL INFORMATION:
;  APPLICANT: PETERSEN, CAROLYN
;  APPLICANT: LEECH, JAMES
;  APPLICANT: NELSON, RICHARD, C.
;  APPLICANT: GUT, JIRI
;  TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
;  TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
;  TITLE OF INVENTION: INFECTIONS
;  FILE REFERENCE: 480.19-4(HV)
;  CURRENT APPLICATION NUMBER: US/08/700,651B
;  CURRENT FILING DATE: 1997-08-14
;  EARLIER APPLICATION NUMBER: 08/415,751
;  EARLIER FILING DATE: 1995-04-03
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 175
;   TYPE: PRT
;   ORGANISM: Cryptosporidium parvum
;   FEATURE:
;   OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-12

  Query Match             5.8%;  Score 129;  DB 3;  Length 175;
  Best Local Similarity   27.3%;  Pred. No. 0.00036;
  Matches   35;  Conservative   15;  Mismatches   74;  Indels    4;  Gaps    1;

Qy        226 LPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLIST 285
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Qy        286 VFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSN 345
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Db         63 TTTTTTTTTTTTTTTTTTTTTKKPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 122

Qy        346 VESSTMNK 353
               ::|  |
Db        123 TTTTTTTK 130


RESULT 15
US-08-928-361B-17
; Sequence 17, Application US/08928361B
; Patent No. 6071518
;  GENERAL INFORMATION:
;    APPLICANT:  Petersen, Carolyn
;    TITLE OF INVENTION:  PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
;    TITLE OF INVENTION:  THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
;    TITLE OF INVENTION:  FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
;    TITLE OF INVENTION:  SPECIES INFECTIONS
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETERS, VERNY, JONES & BIKSA
;      STREET:  385 Sherman Avenue, Suite 6
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306-1840
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/928,361B
;      FILING DATE:  12-SEP-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/026,062
;      FILING DATE:  13-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verny, Hana
;      REGISTRATION NUMBER:  30,518
;      REFERENCE/DOCKET NUMBER:  480.76-1(HV)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-324-1677
;      TELEFAX:  650-324-1678
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  175 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-928-361B-17

  Query Match             5.8%;  Score 129;  DB 3;  Length 175;
  Best Local Similarity   27.3%;  Pred. No. 0.00036;
  Matches   35;  Conservative   15;  Mismatches   74;  Indels    4;  Gaps    1;

Qy        226 LPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLIST 285
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Db          7 IPYTKCVGVKHTTTTTTTTTTTTTTTTTTTTTTTT----TTTTTTTTTTTTTTTTTTTT 62

Qy        286 VFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSN 345
              |     |      ||   ||| : || :  :   |    |  :   |  |       |  : :
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Qy        346 VESSTMNK 353
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Db        123 TTTTTTTK 130


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Job time : 57 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 26, 2005, 21:53:41 ; Search time 1465 Seconds
(without alignments)
97.906 Million cell updates/sec

Title: US-10-735-014-83
Perfect score: 2211
Sequence: 1 MFFGGEGSLTYTLVIICFLT.....LRRKRYSRLDYLINGIYVDI 431

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2211	100.0	431	9	US-09-866-028-83	Sequence 83, Appl
2	2211	100.0	431	9	US-09-989-722-515	Sequence 515, App
3	2211	100.0	431	9	US-09-989-723-515	Sequence 515, App
4	2211	100.0	431	9	US-09-989-279-515	Sequence 515, App
5	2211	100.0	431	9	US-09-989-727-515	Sequence 515, App
6	2211	100.0	431	9	US-09-944-449-83	Sequence 83, Appl
7	2211	100.0	431	9	US-09-989-731-515	Sequence 515, App
8	2211	100.0	431	9	US-09-944-457-83	Sequence 83, Appl
9	2211	100.0	431	9	US-09-944-862-83	Sequence 83, Appl
10	2211	100.0	431	9	US-09-989-732-515	Sequence 515, App
11	2211	100.0	431	9	US-09-991-073-515	Sequence 515, App
12	2211	100.0	431	9	US-09-945-587-83	Sequence 83, Appl
13	2211	100.0	431	9	US-09-990-442-515	Sequence 515, App
14	2211	100.0	431	9	US-09-991-163-515	Sequence 515, App
15	2211	100.0	431	9	US-09-945-015-83	Sequence 83, Appl
16	2211	100.0	431	9	US-09-944-396-83	Sequence 83, Appl
17	2211	100.0	431	9	US-09-993-604-515	Sequence 515, App
18	2211	100.0	431	9	US-09-990-456-515	Sequence 515, App
19	2211	100.0	431	9	US-09-944-432-83	Sequence 83, Appl
20	2211	100.0	431	9	US-09-943-762-83	Sequence 83, Appl
21	2211	100.0	431	9	US-09-944-654-83	Sequence 83, Appl
22	2211	100.0	431	9	US-09-989-721-515	Sequence 515, App
23	2211	100.0	431	9	US-09-943-851A-83	Sequence 83, Appl
24	2211	100.0	431	9	US-09-944-413-83	Sequence 83, Appl
25	2211	100.0	431	9	US-09-992-598-515	Sequence 515, App
26	2211	100.0	431	9	US-09-944-403-83	Sequence 83, Appl
27	2211	100.0	431	9	US-09-944-896-83	Sequence 83, Appl
28	2211	100.0	431	9	US-09-944-944-83	Sequence 83, Appl
29	2211	100.0	431	9	US-09-989-293A-515	Sequence 515, App
30	2211	100.0	431	9	US-09-989-735-515	Sequence 515, App
31	2211	100.0	431	9	US-09-990-444-515	Sequence 515, App
32	2211	100.0	431	9	US-09-944-929-83	Sequence 83, Appl
33	2211	100.0	431	9	US-09-991-181-515	Sequence 515, App
34	2211	100.0	431	9	US-09-989-730-515	Sequence 515, App
35	2211	100.0	431	9	US-09-944-907-83	Sequence 83, Appl
36	2211	100.0	431	9	US-09-990-436-515	Sequence 515, App
37	2211	100.0	431	9	US-09-993-687-515	Sequence 515, App
38	2211	100.0	431	10	US-09-989-734-515	Sequence 515, App
39	2211	100.0	431	10	US-09-997-653-515	Sequence 515, App
40	2211	100.0	431	10	US-09-989-724-515	Sequence 515, App
41	2211	100.0	431	10	US-09-989-728-515	Sequence 515, App
42	2211	100.0	431	10	US-09-990-441-515	Sequence 515, App
43	2211	100.0	431	10	US-09-993-667-515	Sequence 515, App
44	2211	100.0	431	10	US-09-997-428-515	Sequence 515, App
45	2211	100.0	431	10	US-09-997-666-515	Sequence 515, App

ALIGNMENTS

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RESULT 1
US-09-866-028-83
; Sequence 83, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/866,028
;  CURRENT FILING DATE:  2001-05-25
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 83
;   LENGTH: 431
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-866-028-83

  Query Match             100.0%;  Score 2211;  DB 9;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-172;
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Qy        421 DYLINGIYVDI 431
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RESULT 2
US-09-989-722-515
; Sequence 515, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C63
;  CURRENT APPLICATION NUMBER: US/09/989,722
;  CURRENT FILING DATE:  2001-11-19
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.1e-172;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
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Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
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Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
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Db        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
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Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
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Db        421 DYLINGIYVDI 431
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RESULT 3
US-09-989-723-515
; Sequence 515, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher

; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.1e-172;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
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Qy        421 DYLINGIYVDI 431
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Db        421 DYLINGIYVDI 431
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RESULT 4
US-09-989-279-515
; Sequence 515, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.1e-172;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-989-727-515
; Sequence 515, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.1e-172;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
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Qy        421 DYLINGIYVDI 431
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Db        421 DYLINGIYVDI 431
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RESULT 6
US-09-944-449-83
; Sequence 83, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,449
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028

; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
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; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: Decemberl, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 83
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-449-83

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.1e-172;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
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Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
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Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
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Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
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Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
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Qy        421 DYLINGIYVDI 431
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RESULT 7
US-09-989-731-515
; Sequence 515, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690

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;  PRIOR FILING DATE: 1998-06-25
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;  PRIOR APPLICATION NUMBER: 60/091544
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;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

  Query Match             100.0%;  Score 2211;  DB 9;  Length 431;
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Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
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Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
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Db        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
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RESULT 8
US-09-944-457-83
; Sequence 83, Application US/09944457
; Patent No. US20020110859A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,457
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
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;  PRIOR FILING DATE: December 12, 1997
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;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
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;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
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;  PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: December1, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 83
;   LENGTH: 431
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-944-457-83

  Query Match             100.0%;  Score 2211;  DB 9;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-172;
  Matches  431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60

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Qy        421 DYLINGIYVDI 431
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Db        421 DYLINGIYVDI 431


RESULT 9
US-09-944-862-83
; Sequence 83, Application US/09944862
; Patent No. US20020115145A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,862
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,694
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,702
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/069,873
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
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; PRIOR FILING DATE: No. US20020115145A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020115145A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 83
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-862-83

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.1e-172;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
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Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
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Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
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Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
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Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
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Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
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RESULT 10
US-09-989-732-515
; Sequence 515, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.1e-172;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
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Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
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Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
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Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
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Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
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Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

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Db        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
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Qy        421 DYLINGIYVDI 431
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Db        421 DYLINGIYVDI 431


RESULT 11
US-09-991-073-515
; Sequence 515, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C15
;  CURRENT APPLICATION NUMBER: US/09/991,073
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;

Best Local Similarity 100.0%; Pred. No. 2.1e-172;
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RESULT 12
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; Sequence 83, Application US/09945587
; Patent No. US20020127643A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
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; PRIOR FILING DATE: February 28, 2001
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US-09-945-587-83

Query Match 100.0%; Score 2211; DB 9; Length 431;

Best Local Similarity 100.0%; Pred. No. 2.1e-172;
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.1e-172;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
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Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
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Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
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Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
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Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
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Qy        421 DYLINGIYVDI 431
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RESULT 14
US-09-991-163-515
; Sequence 515, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.1e-172;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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; Sequence 83, Application US/09945015
; Patent No. US20020132768A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/945,015
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,694
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,702
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/069,873
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
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;  PRIOR APPLICATION NUMBER: PCT/US99/28301
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;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
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;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
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;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
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US-09-945-015-83

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  Best Local Similarity  100.0%;  Pred. No. 2.1e-172;
  Matches  431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy          421 DYLINGIYVDI 431
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Db          421 DYLINGIYVDI 431
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Search completed: April 26, 2005, 22:25:34
Job time : 1467 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 26, 2005, 21:38:57 ; Search time 52 Seconds
(without alignments)
797.489 Million cell updates/sec

Title: US-10-735-014-83
Perfect score: 2211
Sequence: 1 MFFGGEGSLTYTLVIICFLT.....LRRKRYSRLDYLINGIYVDI 431

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	160.5	7.3	477	2	S53362	mucin 5AC (clone J
3	155.5	7.0	770	2	T22808	hypothetical prote
4	154.5	7.0	851	2	T22696	hypothetical prote
5	154	7.0	534	2	T39903	serine-rich protei
6	151.5	6.9	1251	2	T21389	hypothetical prote
7	150.5	6.8	797	1	VGBEX1	glycoprotein X pre
8	150.5	6.8	860	2	JC4566	chitinase (EC 3.2.
9	149.5	6.8	3020	2	A43932	mucin 2 precursor,
10	149.5	6.8	3570	2	T45025	mucin MUC5B, trach
11	147.5	6.7	790	2	T34293	hypothetical prote
12	147.5	6.7	1609	2	S25345	probable membrane
13	147	6.6	662	2	A45155	mucin FIM-C.1 - Af
14	146	6.6	786	1	A47547	serine proteinease
15	144.5	6.5	505	2	B46629	mucin 6, gastric (
16	144.5	6.5	1104	2	S59310	probable membrane
17	143	6.5	626	2	S53871	Pmel 17 protein -
18	142.5	6.4	377	2	A48018	mucin 7 precursor,
19	142.5	6.4	491	2	A49179	melanoma antigen h
20	142.5	6.4	866	2	T45462	membrane glycoprot
21	142.5	6.4	867	2	T45463	membrane glycoprot
22	141.5	6.4	1161	2	S57180	probable membrane
23	141	6.4	1777	2	T34369	hypothetical prote
24	140	6.3	292	2	S24169	mucin - rat
25	140	6.3	1275	2	T33369	hypothetical prote
26	138	6.2	909	1	QRXLL2	LDL receptor 2 pre
27	137.5	6.2	1630	2	A53577	ascites sialoglyco
28	137	6.2	528	2	I47141	gastric mucin (clo
29	136.5	6.2	1229	2	T25697	hypothetical prote
30	136	6.2	503	2	S63257	probable membrane
31	136	6.2	796	2	T21460	hypothetical prote
32	135.5	6.1	322	2	A53715	apomucin precursor
33	135.5	6.1	543	2	S35047	mucin JUL7 - human
34	135.5	6.1	1299	2	T47182	hypothetical prote
35	135.5	6.1	2271	2	F90073	hypothetical prote
36	134	6.1	164	2	I53641	mucin 5AC - human
37	133.5	6.0	708	2	T19474	hypothetical prote
38	133.5	6.0	3507	2	T34513	hypothetical prote
39	133	6.0	556	2	S51892	probable membrane
40	133	6.0	610	2	S35049	mucin JER57 - huma
41	133	6.0	636	2	S63131	probable membrane
42	133	6.0	1075	2	S48992	flocculation prote
43	133	6.0	1367	2	S51959	hypothetical prote
44	132	6.0	1162	2	JH0557	exo-alpha-sialidas
45	131	5.9	725	2	A41258	a-agglutinin core

ALIGNMENTS

RESULT 1
T29634
hypothetical protein C12D12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29634
R;Nhan, M.; Hawkins, J.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid C12D12.
A;Reference number: Z20656
A;Accession: T29634
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-825 <NHA>
A;Cross-references: UNIPROT:Q17921; EMBL:U51998; PIDN:AAA96080.1; GSPDB:GN00028; CESP:C
A;Experimental source: strain Bristol N2; clone C12D12
C;Genetics:
A;Gene: CESP:C12D12.1
A;Map position: X
A;Introns: 48/1; 86/3; 137/1; 172/3; 224/3; 253/1; 287/3; 328/2; 454/1; 487/3; 692/1
C;Superfamily: Epstein-Barr virus membrane antigen gp350

Query Match 7.9%; Score 174.5; DB 2; Length 825;
Best Local Similarity 23.7%; Pred. No. 0.00064;
Matches 93; Conservative 40; Mismatches 144; Indels 115; Gaps 17;

```
Qy         52 NEPVYTSTQED-----CINSCCSTKNISGDKACNLMIFDTRK------------------ 88
                 | | :|     |      |     ||:  | | |   : | ||:
Db        363 NTPFFTRNANDTIEIYCTVLSCSSITIDGVK---IQITDTKVVQKVDDISYYIFVNTIAN 419

Qy         89 ------TARQPNCYLFFC-------------PNEEACPLKP--AKGLMSY---RIITDF 123
                  : :|   | ||                |:    | |    |   |    : |
Db        420 PGYHQISLKQQGSYAFFVYGKNKLYSYGYEGGANKPTVVLAPPTTPGPTFYPVTTVSTMS 479

Qy        124 PSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLE 183
                 | | :|:   |           :   || |:  |  : || :    | |    | ||
Db        480 PPTTVTVPTTPTPVP--------TTTNTPPANPTT--ATPTTVG---TSKQTNTISPHLS 526

Qy        184 KLFKMDEASAQLLAYKEKG-------HSQSSQFSSDQEIAHLLPENVSALPATVAVASPH 236
                  :      |  :| :          |: :|| :: : :  :   :|:    | | |
Db        527 TITGSIVTSTPTMAPQTSASPTTTPTHTTASQPTTTKPV--VTTNSVTPSTGTTTVPVP- 583

Qy        237 TTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQA 296
                ||: :|   | |       || |:|     ||||||| ||||| |  | : |    |:
Db        584 TTTGSPTTQTTAPVTKPTVPSSTTQ-----TAPPVTTPTSQPPVTTTSLLTTLTTPTVPV 638

Qy        297 MAT----------------TAVLTTTFQA-----------------PTDSKGSLETIPFT 323
                 |                 |   ||| :|                 ||    :: | | |
Db        639 TTTVVPSSATVPTTPPTTVTVAATTTSKAPVVTTSPTLAPTSPTKLPTSPPSTVGTSP-T 697

Qy        324 EISNLTLNTGNVYNPTALSMSNVESSTMNKTA 355
                :|||  |    |||  | :   :: :| |:
```

```
Db        698 APANLTTPTTAPVNPT--SSTTAPTAPVNPTS 727


RESULT 2
S53362
mucin 5AC (clone JER47) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C;Accession: S53362; S71065
R;Guyonnet-Duperat, V.; Audie, J.P.; Debailleul, V.; Laine, A.; Buisine, M.P.; Galiegue-
Biochem. J. 305, 211-219, 1995
A;Title: Characterization of the human mucin gene MUC5AC: a consensus cysteine-rich doma
A;Reference number: S53361; MUID:95126907; PMID:7826332
A;Accession: S53362
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-477 <GUY>
A;Cross-references: UNIPROT:Q14887; EMBL:Z34277
A;Experimental source: clone JER47
R;Porchet, N.
submitted to the EMBL Data Library, June 1994
A;Reference number: S71065
A;Accession: S71065
A;Molecule type: mRNA
A;Residues: 1-211,'S',213-224,'AR',227-259,'S',261-477 <POR>
A;Cross-references: EMBL:Z34277; NID:g563374; PIDN:CAA84031.1; PID:g563375
A;Experimental source: clone JER47
C;Genetics:
A;Gene: GDB:MUC5AC
A;Cross-references: GDB:454136; OMIM:158373
A;Map position: 11p15.5-11p15.5
C;Keywords: glycoprotein; tandem repeat

  Query Match             7.3%;  Score 160.5;  DB 2;  Length 477;
  Best Local Similarity   23.8%;  Pred. No. 0.0028;
  Matches   76;  Conservative   41;  Mismatches  117;  Indels   85;  Gaps   13;

Qy        147 SQAVTPLAHHHTDYSKPTDISW---------RDTLSQKFGSSDHL----EKLFKMD---- 189
              || ||   |    ::| |: :          ::| :    | : :    |:: ::
Db         15 SQPVTRDCHLRCTWTKWFDVDFPSPGPHGGDKETYNNIIRSGEKICRRPEEITRLQCRAE 74

Qy        190 ---EASAQLLAY-----KEKG-----HSQSSQFSS--DQEIAHLLPENVSALPATVAVAS 234
                | | : |       :|:|       |   |    : |:  |  |     | |   ::
Db         75 SHPEVSIEHLGQVVQCSREEGLVCRNQDQQGPFKMCLNYEVRVLCCETPKGCPVT---ST 131

Qy        235 PHTTSATPKPATLLPTNAS----------VTPSGTSQPQLATTAPPVTTVTSQPPTTLI 283
              | |  :||       || ::           || | || || :||: | |: || | |:
Db        132 PVTAPSTPSGRATSPTQSTSSWQKSRTTTLVTTSTTSTPQTSTTSAPTTSTTSAPTTSTT 191

Qy        284 STVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLET------------IPFTEISNLTL 330
              |   |  :| |  ::|  |:|  ||| |  |  |              | |  :: |
Db        192 SAPTTSTTSTPQTSISSAPTTSTTSAPTSSTISRATTSIISAPTTSTTSFPTTSTTSAT- 250

Qy        331 NTGNVYNPTALSMSNVE----SSTMNKTASWEGREASP----------GSSSQGSVPEN 375
                |     ||  : |  :    |:  : | |  |   ||           |:|  || :
Db        251 TTSTTSAPTTSTTSTPQTSKTSAATSSTTSGSGTTPSPVTTTSTASVSKTSTSHVSVSKT 310

Qy        376 QYGLP----------FEKW 384
              :  |          : ||
Db        311 THSQPVTRDCHPRCTWTKW 329


RESULT 3
T22808
hypothetical protein F56H9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22808
R;Burton, J.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19618
A;Accession: T22808
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-770 <WIL>
A;Cross-references: UNIPROT:Q20908; EMBL:Z74473; PIDN:CAA98949.1; GSPDB:GN00023; CESP:F5
A;Experimental source: clone F56H9
C;Genetics:
A;Gene: CESP:F56H9.1
A;Map position: 5
A;Introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2

  Query Match             7.0%;  Score 155.5;  DB 2;  Length 770;
  Best Local Similarity   32.7%;  Pred. No. 0.011;
  Matches   48;  Conservative   16;  Mismatches   64;  Indels   19;  Gaps    5;

Qy        219 LPENVSALPATVAVASPHTTSATPKPATLLPTNASVT-----PSGTSQPQLATTAPPV-- 271
              :|   ::   |  |  | ||::|    |: ||  | |     |  |:    || ||
Db         93 VPPTTTSTTTTTTV--PPTTTSTTTTTTVPPTTTSSTTTTTVPPTTTSSTTTTTVPPTTT 150

Qy        272 --TTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLT 329
                || |: ||||  :|  |   ||     ||:  |||   || |  :  |:| |  | |
Db        151 TSTTTTTVPPTTTSTTTTTTVPAT-----TTSTATTTTVPPTTSTTTTTTVPPTTTSTTT 205

Qy        330 LNTGNVYNPTALSMSNVESSTMNKTAS 356
                |     ||  | :   ::|   | :
Db        206 TTT---VPPTTTSSTTTTTTTTLPTTT 229


RESULT 4
T22696
hypothetical protein F55B11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22696
R;Ainscough, R.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19601
A;Accession: T22696
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-851 <WIL>
A;Cross-references: UNIPROT:O17893; EMBL:Z83318; PIDN:CAB05903.1; GSPDB:GN00022; CESP:F5
A;Experimental source: clone F55B11
C;Genetics:
A;Gene: CESP:F55B11.3
A;Map position: 4
A;Introns: 49/3; 123/3; 226/1; 282/3; 669/3; 743/3

  Query Match             7.0%;  Score 154.5;  DB 2;  Length 851;
  Best Local Similarity   26.6%;  Pred. No. 0.014;
  Matches   47;  Conservative   26;  Mismatches   89;  Indels   15;  Gaps    4;

Qy        219 LPENVSALPATVAVAS------PHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVT 272
              :|   : :| |       |     | ||:  |   | :||  :  |: |:    || | |
Db        377 VPTTTTTVPTTTTTVSTTTTTVPTTTTTVPTTTTTVPTTTTTVPTTTSVPTTTTTVPTT 436

Qy        273 TVTSQPPTTLISTVFTRAAATLQAMA--TTAVLTTTFQAPTDS---KGSLETIPFTEIS- 326
              | |     || :||  |     |   ::  || | |||   || :     :  |:| | |
Db        437 TTTVPTTTTTVSTTTTVPTTTTTVSTTTTVPTTTTTVPTTTTTVPTTTTVPTTTSV 496

Qy        327 ---NLTLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSVPENQYGLP 380
                 |: |     ||  :  :  ::|:  | :      :  |::  :||     :|
Db        497 PTTTTTVPTTTTTVPTTTTTVSTTTTVPTTTTVPTTTTTVSTTTTVPTTTTTVP 553


RESULT 5
T39903
serine-rich protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39903
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z21889
A;Accession: T39903
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-534 <LYN>
A;Cross-references: UNIPROT:O94317; EMBL:AL033534; PIDN:CAA22127.1; GSPDB:GN00067; SPDB:
A;Experimental source: strain 972h-; cosmid c215
C;Genetics:
A;Gene: SPDB:SPBC215.13
A;Map position: 2
C;Superfamily: pig submaxillary mucin

  Query Match             7.0%;  Score 154;  DB 2;  Length 534;
  Best Local Similarity   21.1%;  Pred. No. 0.0087;
  Matches   86;  Conservative   79;  Mismatches  183;  Indels   60;  Gaps   13;

Qy          9 LTYTLVII---------CFLTLRLSASQNCLKKSLEDVV-IDIQSSLSK--GIR------ 50
Db          5 LLFSLICVFCISNIFTQAFLVHQIYGNSSFTKISLNQLEGRDSQEELQRRQEIRYYGRAA 64

Qy         51 --GNEPVY------TSTQEDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCP- 101
Db         65 ETGGTPTYYGYATPTSSSEPSIFSESATPSETNSYSSPVSSYSDPATSQLPSSTSFFSPT 124

Qy        102 --------NEEACPLKPAKGLMSYRIITDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPL 153
Db        125 SSEYTPSSTESSSLLDPSS--VSSAILPSSTSVEVSISSSSLSSSDPLTSSTFSSLSS-- 180

Qy        154 AHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQ 213
Db        181 ---STSSSQP---SVSSTSSSTFSSAAPTSTSSSYLSSSSVVSSSSSPSSSSSSTLTSSS 234

Qy        214 EIAHLLPENVSALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTT 273
Db        235 LSTSSIPSTSSSSSSTSSSLSSSSSSSTASSSSSSSSIISSSSSSSSSPTSTSSTISSSS 294

Qy        274 VTSQPPTTLISTVFTRA------AATLQAMATTAVLTTTF-QAPTDSKGSLETIPFTEIS 326
Db        295 SSSSSPTSTSSTISSSSSSSSSFSSTLSSSSMSS--SSSFSSSPTSSSSTISSSSSSPSS 352

Qy        327 NLTLNT------GNVYNPTALSMSNVESSTMNKTASWEGREASPGSSS 368
Db        353 SSFSSTTSSSKSSSSFSSTVSSSSSTSSSTLTSSSSSSSRPASSSSHS 400


RESULT 6
T21389
hypothetical protein F26C11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21389
R;Matthews, P.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19416
A;Accession: T21389
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1251 <WIL>
A;Cross-references: UNIPROT:Q09550; EMBL:Z47072; PIDN:CAA87369.1; GSPDB:GN00020; CESP:F2
A;Experimental source: clone F26C11
C;Genetics:
A;Gene: CESP:F26C11.3
A;Map position: 2
A;Introns: 24/1; 111/1; 208/1; 272/1; 380/1; 394/3; 485/3; 586/3; 630/3; 669/3; 713/3; 7

  Query Match             6.9%;  Score 151.5;  DB 2;  Length 1251;
  Best Local Similarity   22.4%;  Pred. No. 0.037;
  Matches   93;  Conservative   46;  Mismatches  161;  Indels  115;  Gaps   17;

Qy         17 CFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQEDCI------------ 64
Db         82 CDCVLTSSSTETGTVKFLDREFFRVFSSAEIASTTSLPTTTSPSLNCYWLSEPSNFSEWI 141

Qy         65 ----------NSCCSTKNI----SGDKACNLMIFDTRKTARQPNCY--LFFC-PNEEACP 107
Db        142 DGKQTNLRYNGGCCSETSIQVLNSSDS--TRWILTTSDSWNKANALINLLYCTPN--ACP 197

Qy        108 LKPAKGLMSYRIITDFPSLT----RNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKP 163
Db        198 QQSMLWTNCSNLSTTTSSSTMLSSTTLLTTETETRESSSTGS-TQTTTPSTEPSTTITTP 256

Qy        164 TDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENV 223
Db        257 ME-------------------------------------QSSTVSS------------ 265

Qy        224 SALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLI 283
Db        266 --------VQKTRTSEDKPSSSTTVPTSASTSESSTSSP-MAETSSSSTTSQSSPAST-- 314

Qy        284 STVFTRAAATLQAMATTAV--LTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTAL 341
Db        315 STV--PESSTVGSTPTTGLTTLSTNEQSTSTSSGGHSTSTFGTTSE-TPETSTDFTATST 371

Qy        342 S--------MSNVESSTMNKTASWEGREASPGSSSQGSVPENQYGLPF--EKWLL 386
Db        372 SSSSDSSTQSSNAQTSTIENGSTTTNFTSAPSTSSTPATPTTTYNWPTGGTTWML 426


RESULT 7
VGBEX1
glycoprotein X precursor - equine herpesvirus 1 (strain Ab4p)
C;Species: equine herpesvirus 1
A;Note: host Equus caballus (domestic horse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: H36802
R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
submitted to GenBank, March 1992
A;Description: The DNA sequence of equine herpesvirus-1.
A;Reference number: A36805
A;Accession: H36802
A;Molecule type: DNA
A;Residues: 1-797 <TEL>
A;Cross-references: UNIPROT:P28968; GB:M86664; NID:g330791; PIDN:AAB02506.1; PID:g33086
R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Virology 189, 304-316, 1992
A;Title: The DNA sequence of equine herpesvirus-1.
A;Reference number: A41831; MUID:92295566; PMID:1318606
A;Contents: annotation; possible protein-coding frames
A;Note: neither amino acid nor nucleotide sequence is given
C;Genetics:
A;Gene: 71
C;Superfamily: equine herpesvirus glycoprotein X; equine herpesvirus 1 glycoprotein hom
C;Keywords: glycoprotein; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-797/Product: glycoprotein X #status predicted <MAT>
F;23-465/Region: serine/threonine-rich
F;489-797/Domain: equine herpesvirus 1 glycoprotein homology <EHG>
F;766-790/Domain: transmembrane #status predicted <TMN>
F;590/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             6.8%;  Score 150.5;  DB 1;  Length 797;
  Best Local Similarity   24.3%;  Pred. No. 0.025;
  Matches   58;  Conservative   25;  Mismatches  131;  Indels   25;  Gaps    2;

Qy        158 TDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAH 217
Db         29 TTSSSSTSGSGQSTSSGTTNSSSSPTTSPPTTSSSPPTSTHTSSPSSTSTQSSSTAATSS 88

Qy        218 LLPENVSALPATVAVASPHTTSATPKPATLLPTNASVTP---------------------- 256
Db         89 SAPSTASSTTSIPTSTSTETTTTTPTASTTTPTTTTAAPTTAATTTAVTTAASTSAETTT 148

Qy        257 ---SGTSQPQLAT-TAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTD 312
Db        149 ATATATSTPTTTTPTSTTTTTATTTVPTTASTTTDTTTAATTTAATTTAATTTAATTTAA 208

Qy        313 SKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGS 371
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Db        209 TTTAATTTAATTTAATTSSATTAATTTAATTTAATTTAATTTAATTTAATTTGSPTSGS 267


RESULT 8
JC4566
chitinase (EC 3.2.1.14) 2 precursor - Coccidioides immitis
N;Alternate names: chitin hydrolase homolog; CTS2 protein
C;Species: Coccidioides immitis
C;Date: 12-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 13-Nov-1998
C;Accession: JC4566
R;Pishko, E.J.; Kirkland, T.N.; Cole, G.T.
Gene 167, 173-177, 1995
A;Title: Isolation and characterization of two chitinase-encoding genes (cts1, cts2) fro
A;Reference number: JC4565; MUID:96144270; PMID:8566773
A;Accession: JC4566
A;Molecule type: mRNA
A;Residues: 1-860 <PIS>
A;Cross-references: GB:L41662
C;Genetics:
A;Gene: cts2
A;Introns: 35/3; 181/2
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-22/Domain: signal sequence #status predicted <SIG>
F;22-239/Domain: catalytic #status predicted <CAT>
F;23-860/Product: chitinase 2 #status predicted <MAT>
F;346-682/Region: serine/threonine-rich
F;687-860/Region: cysteine-rich
F;90,657/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             6.8%;  Score 150.5;  DB 2;  Length 860;
  Best Local Similarity   23.9%;  Pred. No. 0.027;
  Matches   78;  Conservative   49;  Mismatches  141;  Indels   59;  Gaps   12;

Qy         65 NSCCSTKN-ISGDKACNLMIFDTRKTARQ---PNCYLFFCPNEEACPLKPAKGLMSYRII 120
              |  || |  ::  |:    : |  |  |:   |   ||
Db        235 NPSCSAKRWVTNPKSVTYTVDDWVKYIRKSGNPLAKLFI---------------------- 273

Qy        121 TDFPSLTRNLPSQE--LPQEDSLLHGQFSQAV-TPLAHHHTDYSKPTDISWRDTLSQ--K 175
                 ||: :    :|| :|  |: :: | | :| : : :     : |  | |:  |
Db        274 --------GLPASKSAAAKEDYLTPGEATKIVSTYMAKYPSTFGGM--MVWEATASENNK 323

Qy        176 FGSSDHL----EKLFKMD---EASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPA 228
               |   :    | | : |     |                :|:|  |:  |   |      : |:
Db        324 LGGLPYADIMKEVLLRCDPDPPTSTVTSTTSASTSTQTSSQSTTMETKTLSASTTPSSPS 383

Qy        229 TVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFT 288
              ||: :|   |::|   :    |  |  |   |:    : :  |||| : :||:| ||   |
Db        384 TVSPSSTMQTTSTGSTSIETVTTRSQEPPSTTISTRSASTEPVTTRSQEPPSTTIS---T 440

Qy        289 RAAA----TLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMS 344
              |:|:    | ::    :   :|: | |::  | :  | | ||  :  ||      |  : |
Db        441 RSASTETVTTRSQEPPSTTISTWSASTETSTSSQDSPSTTISTKSAPTG-----TVTTRS 495

Qy        345 NVESSTMNKTASWEGREASPGSSSQGS 371
                ||   | | |    :  : ||||
Db        496 QDLPSTTISTRSPETETETATTKSQGS 522


RESULT 9
A43932
mucin 2 precursor, intestinal - human (fragments)
N;Alternate names: mucin SMUC-41
C;Species: Homo sapiens (man)
C;Date: 10-Mar-1993 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: A49963; A45106; B45106; A43932; B33532; A61257; PQ0328; PQ0329
R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S.
J. Biol. Chem. 269, 2440-2446, 1994
A;Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the
A;Reference number: A49963; MUID:94132002; PMID:8300571
A;Accession: A49963
A;Molecule type: mRNA
A;Residues: 1-639 <GU1>
A;Cross-references: UNIPROT:Q02817; UNIPROT:Q14884; GB:L21998
R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Rothe, E.M.; Lagace, R.E.; Kim, Y.S.
J. Biol. Chem. 267, 21375-21383, 1992
A;Title: The human MUC2 intestinal mucin has cysteine-rich subdomains located both upstr
A;Reference number: A45106; MUID:93016075; PMID:1400449
A;Accession: A45106
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 626-1895 <GU2>
A;Cross-references: GB:M94131; NID:g186395; PIDN:AAA59163.1; PID:g186396
A;Note: sequence extracted from NCBI backbone (NCBIP:116706)
A;Accession: B45106
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 2037-3020 <GU3>
A;Cross-references: GB:M94132; NID:g186397; PIDN:AAA59164.1; PID:g186398
A;Experimental source: colon
A;Note: sequence extracted from NCBI backbone (NCBIP:116698)
R;Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E.; Hicks, J.W.; Petersen, G.M
J. Clin. Invest. 88, 1005-1013, 1991
A;Title: MUC-2 human small intestinal mucin gene structure. Repeated arrays and polymorp
A;Reference number: A43932; MUID:91358717; PMID:1885763
A;Accession: A43932
A;Molecule type: DNA
A;Residues: 1343-1350,'L',1352-1411,'S',1413-1448,'P',1450-1503,'T',1505-1915 <TOR>
A;Cross-references: GB:M74027; NID:g188863; PIDN:AAA59875.1; PID:g188864
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
R;Gum, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
J. Biol. Chem. 264, 6480-6487, 1989
A;Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and eviden
A;Reference number: A33532; MUID:89197956; PMID:2703501
A;Accession: B33532
A;Molecule type: mRNA
A;Residues: 1916-2193 <GU4>
A;Cross-references: GB:M22405; NID:g188873; PIDN:AAA36334.1; PID:g188874
A;Experimental source: intestine
R;Jany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; Basbaum, C.B.
J. Clin. Invest. 87, 77-82, 1991
A;Title: Human bronchus and intestine express the same mucin gene.
A;Reference number: A61257; MUID:91086481; PMID:1985113
A;Accession: A61257
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'T',1925-1948,'TTS',1952-1954 <JAN>
A;Experimental source: bronchus
R;Xu, G.; Huan, L.; Khatri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; Forstner,
Biochem. Biophys. Res. Commun. 183, 821-828, 1992
A;Title: Human intestinal mucin-like protein (MLP) is homologous with rat MLP in the C-t
A;Reference number: PQ0328; MUID:92198477; PMID:1550588
A;Accession: PQ0328
A;Molecule type: mRNA
A;Residues: 2328-2468 <XUG>
A;Cross-references: GB:M86523
A;Experimental source: small intestine
A;Accession: PQ0329
A;Molecule type: protein
A;Residues: 2328-2342,'K',2344-2354 <XUG1>
C;Genetics:
A;Gene: GDB:MUC2
A;Cross-references: GDB:120203; OMIM:158370
A;Map position: 11p15.5-11p15.5
C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von
C;Keywords: glycoprotein; intestine; tandem repeat
F;2766-2834/Domain: von Willebrand factor type C repeat homology <VWC>

  Query Match             6.8%;  Score 149.5;  DB 2;  Length 3020;
  Best Local Similarity   34.1%;  Pred. No. 0.15;
  Matches   43;  Conservative   12;  Mismatches   52;  Indels   19;  Gaps    4;

Qy        220 PENVSALPATVAVASPHTTSATPKPATL--LPTNASVTP--SGTSQPQLATTAPPVTTVT 275
                | : : || |   : | ||: || | |    ||   :||  | |: |   | :|| || |
Db       1511 PASTTTLPPTTTPSPPTTTTTTPPPTTTPSPPTTTPITPPTSTTTLPPTTTPSPPPTTTT 1570
```

```
Qy        276 SQPPTTLIS------------TVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFT 323
              : ||||  |             |  |    |  :  ||   |||   || :     | | |
Db       1571 TPPPTTTPSPPTTTTPSPPTITTTTPPPTTTPSPPTT---TTTTPPPTTTPSPPTTTPIT 1627

Qy        324 EISNLT 329
                :: |
Db       1628 PPTSTT 1633


RESULT 10
T45025
mucin MUC5B, tracheobronchial [imported] - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45025
R;Desseyn, J.L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A.
J. Biol. Chem. 272, 3168-3178, 1997
A;Title: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various alternat
A;Reference number: Z22899; MUID:97166151; PMID:9013550
A;Accession: T45025
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3570 <DES>
A;Cross-references: EMBL:Z72496; NID:g1834502; PIDN:CAA96577.1; PID:g1834503
A;Experimental source: placenta
C;Genetics:
A;Gene: MUC5B

  Query Match             6.8%;  Score 149.5;  DB 2;  Length 3570;
  Best Local Similarity   30.5%;  Pred. No. 0.19;
  Matches   62;  Conservative   22;  Mismatches   58;  Indels   61;  Gaps   10;

Qy        204 SQSSQFSSDQEIAHLLPENVSALPATVAVA-SPHTTSATPKPATLLPTNASVTPSGTSQP 262
              |::: |||        |   :||||  : | :|  || |  |:: |          ||:
Db        626 SKATPFSS--------PGTATALPALRSTATTPTATSFTAIPSSSL---------GTTWT 668

Qy        263 QLATTAPPVTTV-----TSQPPTTLISTVFTRAAATLQAMA-------------TTAVLT 304
              :|: |  |: |:     :| | |   ||| |  | |  |              || |||
Db        669 RLSQTTTPMATMSTATPSSTPETVHTSTVLTTTATTTGATGSVATPSSTPGTAHTTKVLT 728

Qy        305 TT---FQA-PTDSKGSLETIPFTEISNLTLNT------------GNVYNPTALSMSNVES 348
              ||   | | |: | |   |:|   ||  | |             |  : || |: :
Db        729 TTTTGFTATPSSSPGRARTLP-VWISTTTTPTTRGSTVTPSSIPGTTHTPTVLTTTTTTV 787

Qy        349 STMNKTASWEGREASPGSSSQGS 371
              :|        |  |:| ||:| |
Db        788 AT--------GSMATPSSSTQTS 802


RESULT 11
T34293
hypothetical protein F49E10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34293
R;Miller, N.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid F49E10.
A;Reference number: Z21500
A;Accession: T34293
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-790 <MIL>
A;Cross-references: UNIPROT:Q20599; EMBL:U53341; PIDN:AAC69106.1; GSPDB:GN00028; CESP:F4
A;Experimental source: strain Bristol N2; clone F49E10
C;Genetics:
A;Gene: CESP:F49E10.2
A;Map position: X
A;Introns: 51/1; 92/3; 176/3; 235/3; 332/2; 514/1; 543/2; 569/3; 677/1; 732/3

  Query Match             6.7%;  Score 147.5;  DB 2;  Length 790;
  Best Local Similarity   25.6%;  Pred. No. 0.039;
  Matches   60;  Conservative   34;  Mismatches  107;  Indels   33;  Gaps   11;

Qy        152 PLAHHHTDYSKPTDISWRDTLSQKF--GSSDH--LEKLFKMDEASAQLLAYKEKGHSQSS 207
              |   |:  :||  |:     | : |  | | :  :||  |   |:  |        : |:
Db        537 PFGFHNRFFSK-KDLG----LPEGFQVGQSQYRPIEK--KQGFATLPLRKVSTVPPTTST 589

Qy        208 QFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATT 267
              :: |:      |   : :|:|   ::  ||: |||| |   |: | | : |:       ||
Db        590 SSTTTQK-----PSTTTTVPSTTPTSTTTTTTTTPKPTTSTSTSTSTTTTTTSTTATTT 644

Qy        268 APPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQA-----PTDSKGSLETIPF 322
              | || ||: | || :  :|     |      |   : ||         |    || |  |:
Db        645 PQPTTTTTSEKPVTLTTQTWTAPPTTTVKRTTPQTVPTTTPKIPRWWPLAGSGSTEQ-PW 703

Qy        323 TEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSVPENQ 376
              :     : ||     |    :|      : | :       | | : |   :|| :
Db        704 WQ----KVQTGQNTLPPLFPVSKRVEEKVEKVS------AKP-NESDNKIPEQK 746


RESULT 12
S25345
probable membrane protein YCR089w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YCR1102
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S25345; S19504
R;Wilson, C.; Grisanti, P.; Frontali, L.
Yeast 8, 569-575, 1992
A;Title: The complete sequence of a 6146 bp fragment of Saccharomyces cerevisiae chromo
A;Reference number: S25345; MUID:92397594; PMID:1523889
A;Accession: S25345
A;Molecule type: DNA
A;Residues: 1-1609 <WIL>
A;Cross-references: UNIPROT:P25653; GB:X59720; EMBL:S43845; NID:g1907116; PIDN:CAA42254
R;Frontali, L.; Grisanti, P.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19504
A;Accession: S19504
A;Molecule type: DNA
A;Residues: 1-1609 <FRO>
A;Cross-references: EMBL:X59720; NID:g1907116; PID:e264634; PID:g1907227; MIPS:YCR089w
C;Genetics:
A;Gene: SGD:FIG2
A;Cross-references: SGD:S0000685; MIPS:YCR089w
A;Map position: 3R
C;Keywords: transmembrane protein
F;4-20/Domain: transmembrane #status predicted <TM1>
F;1592-1609/Domain: transmembrane #status predicted <TM2>

  Query Match             6.7%;  Score 147.5;  DB 2;  Length 1609;
  Best Local Similarity   22.4%;  Pred. No. 0.095;
  Matches   88;  Conservative   63;  Mismatches  164;  Indels   77;  Gaps   14;

Qy         41 IQSSLSKGIRGNEPVYTSTQEDCINSCCSTKNISGDKACNLMIFDTR----KTARQPNCY 96
              | || |  |  ||  ::|     :|  |  : |     :|    |     ||      |
Db       1057 IMSSSSNVISTNEKPSSTTSPYNFSSGYSLPSSSTPSQYSLSTATTTINGIKTV-----Y 1111

Qy         97 LFFCPNEEACPLKPAKGLMSYRIITDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHH 156
                :|| |   :  |    | | :  | | ::  ||  | |  : :    | | | ::
Db       1112 TTWCPLAEKSTV--AASSQSSRSVDRFVSSSK--PSSSLSQ--TSIQYTLSTATTTISGL 1165

Qy        157 HTDYSKPTDISWRDTLSQKFGSSDHLE-KLFKMDEASAQLLAYKEKGHSQSSQ------F 209
              | |:    :: : ||     :|   : ::     |::  ::      |:||
Db       1166 KTVYTTWCPLTSKSTLGATTQTSSTAKVRITSASSATSTSISLSTSTESESSSGYLSKGV 1225

Qy        210 SSDQEIAHLLPENVSALPATVAVASP----------HTTSATPKPAT-----LLPTNASV 254
              |  |    :|   |: ||:    ||           ||:|:   :|     |||:::|:
Db       1226 CSGTECTQDVPTQ-SSSPASTLAYSPSVSTSSSSSFSTTTASTLTSTHTSVPLLPSSSSI 1284

Qy        255 TPSGTSQPQLATT---APPVTTVTSQPPTTLISTVFTRAAATLQAMA-------TTAVLT 304
              : |  |   | :|   :|  |: |    | : |: |  ::  | : :          ::::|
Db       1285 SASSPSSTSLLSTSLPSPAFTSSTLPTATAVSSSTFIASSLPLSSKSSLSLSPVSSSILM 1344

Qy        305 TTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPT------------------------ 339
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              : | : : |  || ::|   ||  |::| :|  ||
Db       1345 SQFSSSSSSSSSSLASLPSLSISP-TVDTVSVLQPTTSIATLTCTDSQCQQEVSTICNGSN 1403

Qy        340 ---ALSMSNVESSTMNKTASWEGREASPGSSS 368
                  | :    ||:  | :  | |    :||
Db       1404 CDDVTSTATTPPSTVTDTMTCTGSECQKTTSS 1435


RESULT 13
A45155
mucin FIM-C.1 - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: A45155
R;Hauser, F.; Hoffmann, W.
J. Biol. Chem. 267, 24620-24624, 1992
A;Title: P-domains as shuffled cysteine-rich modules in integumentary mucin C.1 (FIM-C.1
A;Reference number: A45155; MUID:93077556; PMID:1447205
A;Accession: A45155
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-662 <HAU>
A;Cross-references: UNIPROT:Q05049; GB:L02115; NID:g214147; PIDN:AAA74725.1; PID:g951460
F;162-202/Domain: trefoil homology <TRF1>
F;307-347/Domain: trefoil homology <TRF2>
F;354-394/Domain: trefoil homology <TRF3>
F;526-566/Domain: trefoil homology <TRF4>
F;573-613/Domain: trefoil homology <TRF5>
F;621-661/Domain: trefoil homology <TRF6>

  Query Match             6.6%;  Score 147;  DB 2;  Length 662;
  Best Local Similarity   26.9%;  Pred. No. 0.033;
  Matches   49;  Conservative   19;  Mismatches   78;  Indels   36;  Gaps    5;

Qy        228 ATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTT--------VTSQPP 279
              :|  ||:  ||  |    |  ||  : | : |: |   || |  ||         |: |
Db        394 STSQVAATKTT--TTPTTTTTPTTTTTTKATTTTPTTTTTTPTTTTTTTTTTKATTTTPT 451

Qy        280 TTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPT 339
              ||  :|  |:|  |    ||   ||| :| | :  :  | | |  :  |  |     ||
Db        452 TTTPTTTTTKATTTTPTTTTTTPTTTTTKATTTTPTTTTTTPTTTTTKATTTT-----PT 506

Qy        340 ALSMSNVESSTMNKTAS-----------------WEGREASPGSSSQGSVPENQ---YG 378
                :  :    :     | |                 | :  | |     |:|: :   |
Db        507 TTTTTTTTTKATTTTTSGECKMEPSKRADCGYPGITESQCRSKGCCFDSSIPQTKWCFYS 566

Qy        379 LP 380
              ||
Db        567 LP 568


RESULT 14
A47547
serine proteinease stubble-stubbloid (EC 3.4.21.-) - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A47547
R;Appel, L.F.; Prout, M.; Abu-Shumays, R.; Hammonds, A.; Garbe, J.C.; Fristrom, D.; Fris
Proc. Natl. Acad. Sci. U.S.A. 90, 4937-4941, 1993
A;Title: The Drosophila Stubble-stubbloid gene encodes an apparent transmembrane serine
A;Reference number: A47547; MUID:93281671; PMID:7685111
A;Accession: A47547
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-786 <APP>
A;Cross-references: UNIPROT:Q05319; GB:L11451; NID:g158511; PIDN:AAA28918.1; PID:g158512
C;Genetics:
A;Gene: Sb-sbd
A;Cross-references: FlyBase:FBgn0003319
C;Superfamily: serine proteinease stubble-stubbloid; trypsin homology
C;Keywords: hydrolase; serine proteinase; transmembrane protein
F;61-77/Domain: transmembrane #status predicted <TMN>
F;543-781/Domain: trypsin homology <TRY>

  Query Match             6.6%;  Score 146;  DB 1;  Length 786;
  Best Local Similarity   21.0%;  Pred. No. 0.048;
  Matches   74;  Conservative   47;  Mismatches  162;  Indels   70;  Gaps    9;

Qy         63 CINS----CCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYR 118
              |::|     | | | :     |::: |  :  :|   |    |   | | ||
Db        164 CVDSFMFGSCCTHNYTD----NIVLPQTAFSYTRPTKPLTLRPRPPAAPYKP-------- 211

Qy        119 IITDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTD----------YSKPTDISW 168
                     :  : : | |       ||  :  : |   ||                ||||
Db        212 -------MISGMTTIERP------HGAGTLVIRPSGPHHQGTLARPHPPPYQSKPT---- 254

Qy        169 RDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSAL-- 226
                | |   ||: |          :|     :       | |   :|:    :    | :
Db        255 --TASDLHGSASHPSSSSSSSSSSNPNSIWHTSTQQQQQQHQQNQQNHWQMTTEPSFITK 312

Qy        227 --------PATVAVASPHTTS------------ATPKPATLLPTNASVTPSGTSQPQLA 265
                     | | : |   |                :| | : :| : | : : ||    |
Db        313 PRPTGWTKPGIVNLPMPARPSKPSKPTKKPIVYDRSPPPPSSVPPSTSTSTTTSTSLIWPA 372

Qy        266 TTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEI 325
              | ||     ::|  :  :::   :::   :  |:   :||    | :     | | |
Db        373 QTHPPQPHRPTRPQLSPGTSLAASSSSHWPSSTTSTTSSTTSTTTTTTTTRRTTTPTTTT 432

Qy        326 SNLTLN--TGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSVPENQ 376
              | | |     ||  : |:  |:| :|| :     :|  ||| | |  :|
Db        433 RRTTTNKPTRPYQRPTTATSSSSTSTTSSKTPTTTRPISSSSSSSSGIVTSSQ 485


RESULT 15
B46629
mucin 6, gastric (3-repeat clone) - human (fragment)
N;Alternate names: MUC6
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B46629
R;Toribara, N.W.; Roberton, A.M.; Ho, S.B.; Kuo, W.L.; Gum, E.; Hicks, J.W.; Gum Jr., J.
J. Biol. Chem. 268, 5879-5885, 1993
A;Title: Human gastric mucin. Identification of a unique species by expression cloning.
A;Reference number: A46629; MUID:93194895; PMID:7680650
A;Accession: B46629
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-505 <TOR>
A;Cross-references: UNIPROT:Q14395; GB:L07518; NID:g292045; PIDN:AAB61945.1; PID:g292046
A;Experimental source: stomach
A;Note: sequence extracted from NCBI backbone (NCBIN:128397, NCBIP:128399)
C;Genetics:
A;Gene: GDB:MUC6
A;Cross-references: GDB:134734; OMIM:158374
A;Map position: 11p15.5-11p15.5
C;Keywords: glycoprotein

  Query Match             6.5%;  Score 144.5;  DB 2;  Length 505;
  Best Local Similarity   23.9%;  Pred. No. 0.035;
  Matches   78;  Conservative   37;  Mismatches  101;  Indels  111;  Gaps   15;

Qy         89 TARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFPSLTRNLPSQELPQEDSLLH-GQFS 147
              ::| |  :    |  : |  : | |:    | | : |   |: |||   | |   ||
Db        116 SSRPPPPFTTHSPPTGSSPFS-STGPMT---ATSFKT-TTTYPTPSLPQTTPLTHVPPFS 170

Qy        148 QA-VTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQS 206
              : |||: |      ||                                        | |
Db        171 TSLVTPITH---TVITPT-------------------------------------HPQ- 188

Qy        207 SQFSSDQEIAHLLPENVSALPATV----------------AVASPHTTSATPKPATLLP 249
                  |   | |    | | ||                  ::  |:: : | | : | |
Db        189 ---MSTSAYIHSTPTGTIASPTTVKATRSTYTAPLMTATTSRISQAHSSISTAKTSTSLH 245

Qy        250 TNAS--------------VTPSGTSQPQLATTAPPVTTVT----SQPPTTLIS----TVF 287
              ::||              |||  ||:     |: |||  |    |:||| : :     |
Db        246 SHASSTHHPEVTPTSTTNVTPKSTSR----DTSTPVTHTTSATSSRPPTPITTHSSPTRS 301
```

```
Qy        288 TRAAATLQAMATTAVLTTTFQAPTDSKGSLET-IPFTEISNLTLNTGNVYNPTALSMSNV 346
              :  ::|    ||:   |||:  |:  : :| | :|    |::| :|  |  ||   ||
Db        302 SPLSSTGPMTATSIKTTTTYPTPSHPQTTLTTHVPPFSTSSVTPSTHTVITPTHAQMST- 360

Qy        347 ESSTMNKTASWEGREASPGSSSQGSVP 373
                          ||  |:  |:||
Db        361 --------------SASIHSTPTGTVP 373
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Search completed: April 26, 2005, 21:52:31
Job time : 55 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 26, 2005, 20:26:45 ; Search time 122 Seconds
(without alignments)
1809.067 Million cell updates/sec

Title: US-10-735-014-83
Perfect score: 2211
Sequence: 1 MFFGGEGSLTYTLVIICFLT.....LRRKRYSRLDYLINGIYVDI 431

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2211	100.0	431	1	MNS1_HUMAN	Q9h8j5 homo sapien
2	2039	92.2	431	1	MNS1_MACFA	Q95kg7 macaca fasc
3	2022	91.5	397	2	Q9NW60	Q9nw60 homo sapien
4	1164.5	52.7	414	1	MNS1_MOUSE	Q9cr33 mus musculu
5	503	22.7	194	2	Q8K0I0	Q8k0i0 mus musculu
6	197.5	8.9	392	2	Q8VCP2	Q8vcp2 mus musculu
7	197	8.9	449	2	Q9H2K4	Q9h2k4 homo sapien
8	196.5	8.9	392	2	Q9D8N1	Q9d8n1 mus musculu
9	188	8.5	449	2	Q96F05	Q96f05 homo sapien
10	180.5	8.2	1349	2	Q8WWQ4	Q8wwq4 homo sapien
11	168	7.6	519	2	Q7YTR7	Q7ytr7 caenorhabdi
12	163	7.4	4262	2	Q685J2	Q685j2 homo sapien
13	163	7.4	4493	2	Q685J3	Q685j3 homo sapien
14	160.5	7.3	477	2	Q14887	Q14887 homo sapien
15	157.5	7.1	2448	2	Q8WWQ5	Q8wwq5 homo sapien
16	156.5	7.1	328	2	O00446	O00446 homo sapien
17	155.5	7.0	769	2	Q17921	Q17921 caenorhabdi
18	154.5	7.0	784	2	Q6CI85	Q6ci85 yarrowia li
19	154	7.0	534	2	O94317	O94317 schizosacch
20	151.5	6.9	1240	1	YQU3_CAEEL	Q09550 caenorhabdi
21	150.5	6.8	382	2	Q9XZZ8	Q9xzz8 litomosoide
22	150.5	6.8	797	1	VGLX_EHV1B	P28968 equine herp
23	150.5	6.8	797	2	Q6DLE0	Q6dle0 equid herpe
24	150.5	6.8	860	1	CHI2_COCIM	P54197 coccidioide
25	149.5	6.8	5179	1	MUC2_HUMAN	Q02817 homo sapien
26	149.5	6.8	5703	1	MU5B_HUMAN	Q9hc84 homo sapien
27	149	6.7	943	1	YL61_SCHPO	Q8tfg9 schizosacch
28	148.5	6.7	791	2	Q66VC3	Q66vc3 equid herpe
29	148.5	6.7	1233	1	MU5A_HUMAN	P98088 homo sapien
30	148	6.7	513	2	Q6V4A2	Q6v4a2 drosophila
31	148	6.7	2299	2	Q6A564	Q6a564 bacteroides
32	147.5	6.7	790	2	Q20599	Q20599 caenorhabdi
33	147.5	6.7	842	2	Q95QF5	Q95qf5 caenorhabdi
34	147.5	6.7	1609	1	FIG2_YEAST	P25653 saccharomyc
35	147	6.6	662	1	MUC1_XENLA	Q05049 xenopus lae
36	146	6.6	316	2	Q8V0M4	Q8v0m4 equid herpe
37	146	6.6	457	2	Q86AK1	Q86ak1 dictyosteli
38	146	6.6	472	2	Q6BHG8	Q6bhg8 debaryomyce
39	146	6.6	786	1	STUB_DROME	Q05319 drosophila
40	145.5	6.6	629	2	Q24017	Q24017 drosophila
41	145.5	6.6	716	2	Q9NYE4	Q9nye4 homo sapien
42	145.5	6.6	901	2	Q6CAJ2	Q6caj2 yarrowia li
43	145	6.6	425	2	Q702W3	Q702w3 human herpe
44	145	6.6	1079	2	Q9N4S7	Q9n4s7 caenorhabdi
45	144.5	6.5	377	2	Q8TAX7	Q8tax7 homo sapien

ALIGNMENTS

RESULT 1
MNS1_HUMAN
ID MNS1_HUMAN STANDARD; PRT; 431 AA.
AC Q9H8J5; Q8NEC1;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE MANSC domain containing protein 1 precursor (UNQ316/PRO361).
GN Name=MANSC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

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RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P., Gray A.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- SIMILARITY: Contains 1 MANSC domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AK023622; BAB14621.1; -.
DR   EMBL; AY358563; AAQ88926.1; -.
DR   EMBL; BC032998; AAH32998.1; -.
DR   Genew; HGNC:25505; MANSC1.
DR   InterPro; IPR011106; MANSC_N.
DR   Pfam; PF07502; MANSC; 1.
DR   PROSITE; PS50986; MANSC; 1.
KW   Glycoprotein; Signal; Transmembrane.
FT   SIGNAL        1     26       Potential.
FT   CHAIN        27    431       MANSC domain containing protein 1.
FT   DOMAIN       27    385       Extracellular (Potential).
FT   TRANSMEM    386    408       Potential.
FT   DOMAIN      409    431       Cytoplasmic (Potential).
FT   DOMAIN       33    117       MANSC.
FT   DOMAIN      237    332       Thr-rich.
FT   CARBOHYD     72     72       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    222    222       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    251    251       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    327    327       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    352    352       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT     55     55       V -> I (in Ref. 3).
SQ   SEQUENCE   431 AA;  46810 MW;  189136416F0F89AE CRC64;

  Query Match             100.0%;  Score 2211;  DB 1;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-136;
  Matches  431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
                ||||||||||
Db        421 DYLINGIYVDI 431


RESULT 2
MNS1_MACFA
ID   MNS1_MACFA     STANDARD;      PRT;   431 AA.
AC   Q95KG7;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   MANSC domain containing protein 1 precursor (QtrA-13483).
GN   Name=MANSC1;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA   Suzuki Y., Sugano S., Hashimoto K.;
RT   "Isolation of full-length cDNA clones from macaque brain cDNA
RT   libraries.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- SIMILARITY: Contains 1 MANSC domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB060888; BAB46892.1; -.
DR   InterPro; IPR011106; MANSC_N.
DR   Pfam; PF07502; MANSC; 1.
DR   PROSITE; PS50986; MANSC; 1.
KW   Glycoprotein; Signal; Transmembrane.
FT   SIGNAL        1     26       Potential.
FT   CHAIN        27    431       MANSC domain containing protein 1.
FT   DOMAIN       27    385       Extracellular (Potential).
```

```
FT   TRANSMEM     386    408       Potential.
FT   DOMAIN       409    431       Cytoplasmic (Potential).
FT   DOMAIN        33    117       MANSC.
FT   DOMAIN       237    332       Thr-rich.
FT   CARBOHYD      31     31       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     222    222       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     251    251       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     327    327       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     352    352       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   431 AA;  47104 MW;  BF10996E87F76C69 CRC64;

  Query Match             92.2%;  Score 2039;  DB 1;  Length 431;
  Best Local Similarity   92.3%;  Pred. No. 5.5e-125;
  Matches  398;  Conservative    9;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
              |||||:||||||||||||||||:|||||| ||||||||||||||||||||||:|||||
Db          1 MFFGGKGSLTYTLVIICFLTLRLAASQNCLNKSLEDVVIDIQSSLSKGIRGNEPIYTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
              |||||||||||| |||||||| ||||||| ||:|||||||||||||||||||||| |||||
Db         61 EDCINSCCSTKIISGDKACNFMIFDTRKIARRPNCYLFFCPNEEACPLKPAKGLRSYRII 120

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
              |||||||||||||||||||| |||||||||| ||  ||||||||||:|| |||||||
Db        121 RDFPSLTRNLPSQELPQEDSLLPGQFSQAVTPLARHHIVYSKPTDISWRETLPQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
              |||||| ||:||||||| |||||||||| ||||||||||||||  ||||||||||||||
Db        181 HLEKLFNMDKASAQLLVYKEKGHSQSSQISSDQEIAHLLPENVSVFPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
              |||||  |||||||||||||||||:|||||||||||||||| |||| |||||||||
Db        241 TPKPAIRLPTNASVTPSGTSQPQLATTSPPVTTVTSQPPTTLISTGFTRAVATLQAMATT 300

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
              |||||||||||| ||||||||||||||||||||||||||||||:||  |||||||||
Db        301 AVLTTTFQAPTDLKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVKSSATNKTASWEGR 360

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
              ||||| ||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EASPGRSSQGNVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy        421 DYLINGIYVDI 431
              ||||||||||
Db        421 DYLINGIYVDI 431


RESULT 3
Q9NW60
ID   Q9NW60      PRELIMINARY;      PRT;   397 AA.
AC   Q9NW60;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein FLJ10298.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA   Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA   Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA   Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA   Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA   Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA   Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA   Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA   Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA   Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
DR   EMBL; AK001160; BAA91526.1; -.
DR   InterPro; IPR011106; MANSC_N.
DR   Pfam; PF07502; MANSC; 1.
SQ   SEQUENCE   397 AA;  43062 MW;  E2FEFF2E61122C62 CRC64;

  Query Match             91.5%;  Score 2022;  DB 2;  Length 397;
  Best Local Similarity   92.1%;  Pred. No. 6.4e-124;
  Matches  397;  Conservative    0;  Mismatches    0;  Indels   34;  Gaps    1;

Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
              |||||||||||||                                 ||||||||||||
Db          1 MFFGGEGSLTYTL---------------------------------GIRGNEPVYTSTQ 26

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 86

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 146

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 206

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 266

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 326

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 386

Qy        421 DYLINGIYVDI 431
              ||||||||||
Db        387 DYLINGIYVDI 397


RESULT 4
MNS1_MOUSE
ID   MNS1_MOUSE     STANDARD;      PRT;   414 AA.
AC   Q9CR33; Q80V71;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   MANSC domain containing protein 1 precursor.
GN   Name=Mansc1;
OS   Mus musculus (Mouse).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cecum, Colon, and Medulla oblongata;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- SIMILARITY: Contains 1 MANSC domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AK018660; BAB31329.1; -.
DR   EMBL; AK018635; BAB31319.1; -.
DR   EMBL; AK033526; BAC28341.1; -.
DR   EMBL; AK033557; BAC28357.1; -.
DR   EMBL; AK046837; BAC32892.1; -.
DR   EMBL; BC039930; AAH39930.1; -.
DR   MGD; MGI:1914979; 9130403P13Rik.
DR   InterPro; IPR011106; MANSC_N.
DR   Pfam; PF07502; MANSC; 1.
DR   PROSITE; PS50986; MANSC; 1.
KW   Glycoprotein; Signal; Transmembrane.
FT   SIGNAL       1    24       Potential.
FT   CHAIN       25   414       MANSC domain containing protein 1.
FT   DOMAIN      25   369       Extracellular (Potential).
FT   TRANSMEM   370   392       Potential.
FT   DOMAIN     393   414       Cytoplasmic (Potential).
FT   DOMAIN      32   116       MANSC.
FT   CARBOHYD   128   128       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   234   234       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   335   335       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT    11    13       SLL -> ALV (in Ref. 2).
FT   CONFLICT    56    56       L -> V (in Ref. 2).
FT   CONFLICT    63    63       I -> V (in Ref. 2).
FT   CONFLICT   139   139       F -> S (in Ref. 2).
FT   CONFLICT   170   170       R -> G (in Ref. 2).
FT   CONFLICT   192   192       M -> T (in Ref. 2).
FT   CONFLICT   242   242       E -> A (in Ref. 2).
FT   CONFLICT   275   275       G -> A (in Ref. 2).
SQ   SEQUENCE   414 AA;  44822 MW;  29BB9197C916BA8E CRC64;

  Query Match           52.7%;  Score 1164.5;  DB 1;  Length 414;
  Best Local Similarity  59.9%;  Pred. No. 6.1e-68;
  Matches  258;  Conservative   37;  Mismatches  119;  Indels   17;  Gaps    6;

Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
              | | |  || |:|::| ||| | || |||| ||||||||||||||||||||||:: :||
Db          1 MLFRGT-SLAYSLLVISFLTPRSSAGQNCLTKSLEDVVIDIQSSLSKGIRGNEPIHLATQ 59

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
              |||| :|||||:|:|||||||||||||| ||||||||||:|:|||||||||::||:|
Db         60 EDCIGACCSTKDIAGDKACNLMIFDTRKTDRQPNCYLFFCPSEDACPLKPAKGLVTYRLI 119

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
               ||| : |   |:| | : ||    |   ||       | ||| :|| |  | |  :
Db        120 RDFPLTSANSSLQQLTQGEFLLLDHSSPGATPGFRTPAGYPKPTGLSWSDRSSLKSTAPL 179

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
              || |  | || | ||   :|| |||| |  |: ::|||||: |   | |||||     ||
Db        180 HLRKHIKADETSMQL--PEEKSHSQSLQLPSELKMAHLLPKTVPTPPTTVAVAPLRNVSA 237

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
              | ||  || |: |||     | : |||| |||||||: |    || ||        :
Db        238 TLKPELLL-TSISVTAKTLKQKE-ATTASPVTTVTSKLPGVPGSTSFT------PVVTHQ 289

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
              | || |||| ||||| |||:||   | ||       :|     |  |||  ||||||| |
Db        290 AALTNTFQAHTDSKGILETMPFQGGSTLT------SDPRHGKSSTSESSITNKTASWEDR 343

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
              | ||:|    |::|:|| |||||||:|| ||||||||||||:| |:|||||||||
Db        344 RVSVGSASLNKGPKSQHGLSFEKWLLIGTLLCGVLFLVIGLVLLGRMLVEALRRKRYSRL 403

Qy        421 DYLINGIYVDI 431
              ||||||||||
Db        404 DYLINGIYVDI 414


RESULT 5
Q8K0I0
ID   Q8K0I0      PRELIMINARY;      PRT;   194 AA.
AC   Q8K0I0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mansc1 protein (Fragment).
```

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GN   Name=Mansc1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Liver;
RA   Director MGC Project;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC031372; AAH31372.1; -.
DR   MGD; MGI:1914979; Mansc1.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
FT   NON_TER       1       1
SQ   SEQUENCE   194 AA;  20701 MW;  11C1F299E1FB3C44 CRC64;

  Query Match             22.7%;  Score 503;  DB 2;  Length 194;
  Best Local Similarity   59.5%;  Pred. No. 3.5e-25;
  Matches  122;  Conservative   13;  Mismatches   56;  Indels   14;  Gaps    4;

Qy        227 PATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTV 286
              | |||||     ||| ||| || |: |||     | : |||| |||||||: |    ||
Db          4 PTTVAVAPLRNVSATLKPALLL-TSISVTAKTLKQKE-ATTASPVTTVTSKLPAVPGSTS 61

Qy        287 FTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNV 346
              ||        :   | || |||| ||||| |||:||   | ||       :|     |
Db         62 FT------PVVTHQAALTNTFQAHTDSKGILETMPFQGGSTLT------SDPRHGKSSTS 109

Qy        347 ESSTMNKTASWEGREASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGR 406
              |||  ||||||| |   | ||:|    |::|:|| |||||||:|| ||||||||||||||
Db        110 ESSITNKTASWEDRRVSVGSASLNKGPKSQHGLSFEKWLLIGTLLCGVLFLVIGLVLLGR 169

Qy        407 ILSESLRRKRYSRLDYLINGIYVDI 431
              :| |:||||||||||||||||||||
Db        170 MLVEALRRKRYSRLDYLINGIYVDI 194


RESULT 6
Q8VCP2
ID   Q8VCP2      PRELIMINARY;      PRT;   392 AA.
AC   Q8VCP2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   1810055G02Rik protein.
GN   Name=1810055G02Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Liver;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019471; AAH19471.1; -.
DR   MGD; MGI:1919306; 1810055G02Rik.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
SQ   SEQUENCE   392 AA;  41081 MW;  1D79796C791211FA CRC64;

  Query Match             8.9%;  Score 197.5;  DB 2;  Length 392;
  Best Local Similarity   26.5%;  Pred. No. 7.3e-05;
  Matches   89;  Conservative   37;  Mismatches  115;  Indels   95;  Gaps   14;

Qy        156 HHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQF------ 209
              | |: | ||          : |::| :          | | |    | | : |
Db         88 HGTNTSTPT---------TREGTTDRV--------TSRTLAAPTSSGPSSAEQTRPTTIA 130

Qy        210 ---SSDQEIAHLLPENVSALPAT--VAVASPHTT------------SATPKPATLLPTN 251
                 |    | :   | |  | |   |  :|||              : || ||   ||:
Db        131 GLPSLSTPHAEVPRTNASVSPRTAMAATVAPHTATLAAGTVNTSDPHTRTPSPAKSTPTD 190

Qy        252 -ASVTPSGTSQPQLATTAPPVTT----------------VTSQPPTTLISTVFTRAAAT 293
               :|  |  ||  |:  |   :||                  | :| || : |    :|:|
Db        191 TSSKNPIPTSGAQIQGTTVQLTTDQPVHSTAGRSALSPSNATLEPTTTQVQTK-EPSAST 249

Qy        294 LQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNK 353
              : | ||:        :||       |:|       |  ||      | |:   | : | :
Db        250 VPARATSLSPDVDVISPTTQPS--PTLP-------TQGTGG--PGTLLTTEQVGTKTTSG 298

Qy        354 TASWEGREASPGSSSQGSV----------PENQYGLPFE--------KWLLIGSLLFGV 394
              |||      | | | | :            : || :  :         | ||:  || ||
Db        299 TAS-----AGPTSRSSGDIKVPTTDSCQPSTQGQYLVTIDALTPSLVNKMLLLVVLLVGV 353

Qy        395 LFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVD 430
              :  ||:      || ::| |:::||||||:| |
Db        354 TLFIAVLVMFALQAYESYKKKDYTQVDYLINGMYAD 389


RESULT 7
Q9H2K4
ID   Q9H2K4      PRELIMINARY;      PRT;   449 AA.
AC   Q9H2K4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

```
DE   DM4E3.
GN   Name=C11orf24;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21295044; PubMed=11401438; DOI=10.1006/geno.2000.6492;
RA   Twells R.C.J., Metzker M.L., Brown S.D., Cox R., Garey C., Hammond H.,
RA   Hey P.J., Levy E., Nakagawa Y., Philips M.S., Todd J.A., Hess J.F.;
RT   "The sequence and gene characterization of a 400-kb candidate region
RT   for IDDM4 on chromosome 11q13.";
RL   Genomics 72:231-242(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Twells R.C., Metzker M.L., Brown S.D., Cox R., Garey C., Hammond H.,
RA   Hey P.J., Levy E., Nakagawa Y., Philips M.S., Todd J.A., Hess J.F.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF264781; AAG36936.1; -.
DR   InterPro; IPR001395; Aldo/ket_red.
DR   PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
SQ   SEQUENCE   449 AA;  46100 MW;  11C8B0FCC3BBF921 CRC64;

  Query Match             8.9%;  Score 197;  DB 2;  Length 449;
  Best Local Similarity   22.2%;  Pred. No. 9.3e-05;
  Matches  117;  Conservative   49;  Mismatches  166;  Indels  196;  Gaps   18;

Qy         13 LVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQEDCINSCCSTKN 72
              ||:|   :| || |          |   :   | |     | |   | ||   :  |
Db          5 LVLIWIFSLSLSESHAASNDPRNFVPNKMWKGLVKRNASVETVDNKTSEDVTMAAAS--- 61

Qy         73 ISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFPSLTRNLPS 132
                                              |:   ||           :   :| |
Db         62 ----------------------------------PVTLTKG----------TSAAHLNS 76

Qy        133 QELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEAS 192
              |:  ||:                  || |:|          :   |::| :  :     ||
Db         77 MEVTTEDT---------------SRTDVSEP---------ATSGGAADGVTSIAPTAVAS 112

Qy        193 AQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHT-----TSATPKPATL 247
              :  |        :  :|   :|   |   :|   |||  :| |     |:|:  | ||
Db        113 STTAA-------SITTAASSMTVASSAP-TTAASSTTVASIAPTTAASSMTAASSTPMTL 164

Qy        248 ---LPTNASV--TPS--GTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
                 ||: |   |||   |  | |:|     |   :: | |  ::|: |||    | :|||
Db        165 ALPAPTSTSTGRTPSTTATGHPSLSTALAQVPKSSALPRTATLATLATRA----QTVATT 220

Qy        301 A---------------------------------------------VLTTTFQAPTDSKG 315
              |                                             | ||   |  |
Db        221 ANTSSPMSTRPSPSKHMPSDTAASPVPPMRPQAQGPISQVSVDQPVVNTTNKSTPMPSNT 280

Qy        316 SLETIPFTEISNLTLNTGNVYNPTAL-------------SMS-NVESSTMNKTASWEG- 359
              : |  |   :  :|         |||             :||   : | |  |     |
Db        281 TPEPAPTPTV--VTTTKAQAREPTASPVPVPHTSPIPEMEAMSPTTQPSPMPYTQRAAGP 338

Qy        360 ----------REASPGSSSQGSVPENQYG--LP-------------------------FE 382
                       ||:||: | |  | :  |  :|                          :
Db        339 GTSQAPEQVETEATPGTDSTGPTPRSSGGTKMPATDSCQPSTQGQYMVVTTEPLTQAVVD 398

Qy        383 KWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVD 430
              | ||:  || ||   :  |||       || ::| |:::||||||:| |
Db        399 KTLLLVVLLLGVTLFITVLVLFALQAYESYKKKDYTQVDYLINGMYAD 446


RESULT 8
Q9D8N1
ID   Q9D8N1      PRELIMINARY;      PRT;   392 AA.
AC   Q9D8N1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
DE   library, clone:1810055G02 product:hypothetical Threonine-rich region
DE   containing protein, full insert sequence.
GN   Name=1810055G02Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK007868; BAB25319.1; -.
DR   MGD; MGI:1919306; 1810055G02Rik.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
KW   Hypothetical protein.
SQ   SEQUENCE   392 AA;  41095 MW;  6BBA958C73489874 CRC64;
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  Query Match             8.9%;  Score 196.5;  DB 2;  Length 392;
  Best Local Similarity   26.1%;  Pred. No. 8.4e-05;
  Matches   88;  Conservative   42;  Mismatches  110;  Indels   97;  Gaps   15;

Qy        156 HHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEI 215
              | |: | ||          : |::| :         ::: ||         |:: :    |
Db         88 HGTNTSTPT---------TREGTTDRV---------TSRTLAVPTSSGPSSAEQTRPTTI 129

Qy        216 AHL---------LPE-NVSALPAT--VAVASPHTT-------------SATPKPATLLPT 250
              | |         :|  | |  | |   |  :|||              : || ||   ||
Db        130 AGLPSLSTPHAEVPRTNASVSPRTAMAATVAPHTATLAAGTVNTSDPHTRTPSPAKSTPT 189

Qy        251 N-ASVTPSGTSQPQLATTAPPVTT-----------------VTSQPPTTLISTVFTRAAA 292
              : :|  |  ||  |:  |   :||                 | :| || : |    :|:
Db        190 DTSSKNPIPTSGAQIQGTTVQLTTDQPVHSTAGRSALSPSNATLEPTTTQVQTK-EPSAS 248

Qy        293 TLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMN 352
              |: | ||:        :||       |:|       |  ||     | |:   | : | :
Db        249 TVPARATSLSPDVDVISPTTQPS--PTLP-------TQGTGG--PGTLLTTEQVGTKTTS 297

Qy        353 KTASWEGREASPGSSSQGSV-----------PENQYGLPFE--------KWLLIGSLLFG 393
              |||     | | | | | :           : || :  :         | ||:  || |
Db        298 GTAS-----AGPTSRSSGDIKVPTTDSCQPSTQGQYLVTIDALTPSLVNKMLLLVVLLVG 352

Qy        394 VLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVD 430
              |   :  ||:      || ::| |:::||||||:| |
Db        353 VTLFIAVLVMFALQAYESYKKKDYTQVDYLINGMYAD 389


RESULT 9
Q96F05
ID   Q96F05      PRELIMINARY;      PRT;   449 AA.
AC   Q96F05;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Chromosome 11 open reading frame 24 (FP2568) (C11orf24).
GN   Name=C11orf24; ORFNames=UNQ1872;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
RA   Wan D.F., Gu J.R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; BC011765; AAH11765.1; -.
DR   EMBL; AF370372; AAQ15208.1; -.
DR   EMBL; AY358754; AAQ89114.1; -.
DR   Genew; HGNC:1174; C11orf24.
DR   InterPro; IPR001395; Aldo/ket_red.
DR   PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
SQ   SEQUENCE   449 AA;  46142 MW;  BF984AA360F6C415 CRC64;

  Query Match             8.5%;  Score 188;  DB 2;  Length 449;
  Best Local Similarity   22.0%;  Pred. No. 0.00036;
  Matches  116;  Conservative   49;  Mismatches  167;  Indels  196;  Gaps   18;

Qy         13 LVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQEDCINSCCSTKN 72
              ||:|   :| || |          |   :   | |     | |   | ||   :  |
Db          5 LVLIWIFSLSLSESHAASNDPRNFVPNKMWKGLVKRNASVETVDNKTSEDVTMAAAS--- 61

Qy         73 ISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFPSLTRNLPS 132
                                              |:   ||          :   :| |
Db         62 ---------------------------------PVTLTKG----------TSAAHLNS 76

Qy        133 QELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEAS 192
               |:  ||:                 || |:|         :    ::| :  :     ||
Db         77 MEVTTEDT--------------SRTDVSEP---------ATSGVAADGVTSIAPTAVAS 112

Qy        193 AQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHT-----TSATPKPATL 247
              :  |          :  :|   :|    |   :|   |||  :| |     |:|:  | ||
Db        113 STTAA-------SITTAASSMTVASSAP-TTAASSTTVASIAPTTAASSMTAASSTPMTL 164

Qy        248 ---LPTNASV--TPS--GTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
                 ||: |   |||    |  | |:|    |   :: | |  ::|: |||    | :|||
Db        165 ALPAPTSTSTGRTPSTTATGHPSLSTALAQVPKSSALPRTATLATLATRA----QTVATT 220

Qy        301 A-----------------------------------------------VLTTTFQAPTDSKG 315
              |                                               | ||    |  |
Db        221 ANTSSPMSTRPSPSKHMPSDTAASPVPPMRPQAQGPISQVSVDQPVVNTTNKSTPMPSNT 280

Qy        316 SLETIPFTEISNLTLNTGNVYNPTAL--------------SMS-NVESSTMNKTASWEG- 359
              : |  |   :  :|     |||                 :||   : | |  |    |
Db        281 TPEPAPTPTV--VTTTKAQAREPTASPVPVPHTSPIPEMEAMSPTTQPSPMPYTQRAAGP 338

Qy        360 ----------REASPGSSSQGSVPENQYG--LP------------------------FE 382
                       ||:||: | |  | :  |  :|                         :
Db        339 GTSQAPEQVETEATPGTDSTGPTPRSSGGTKMPATDSCQPSTQGQYMVVTTEPLTQAVVD 398

Qy        383 KWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVD 430
              | ||:  || ||   :  |||       || ::| |:::||||||:| |
Db        399 KTLLLVVLLLGVTLFITVLVLFALQAYESYKKKDYTQVDYLINGMYAD 446


RESULT 10
Q8WWQ4
ID   Q8WWQ4      PRELIMINARY;      PRT;  1349 AA.
AC   Q8WWQ4;
```

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DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Mucin 5 (Fragment).
GN   Name=MUC5AC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21426417; PubMed=11535137; DOI=10.1042/0264-6021:3580763;
RA   Escande F., Aubert J.P., Porchet N., Buisine M.P.;
RT   "Human mucin gene MUC5AC: organization of its 5'-region and central
RT   repetitive region.";
RL   Biochem. J. 358:763-772(2001).
DR   EMBL; AJ298318; CAC83675.1; -.
FT   NON_TER       1      1
FT   NON_TER    1349   1349
SQ   SEQUENCE   1349 AA;  135599 MW;  4DC3C1544F1E5EBA CRC64;

  Query Match             8.2%;  Score 180.5;  DB 2;  Length 1349;
  Best Local Similarity   21.6%;  Pred. No. 0.0044;
  Matches   88;  Conservative   62;  Mismatches  174;  Indels   83;  Gaps   14;

Qy          4 GGEGSLTYTLVI-----ICFLTLRLSASQNCLKKSLEDVVID-----IQSSLSKGIRGNE 53
              ||:   ||  :|     ||     ::  | |  ||  :| |:     :| |  :|:
Db        517 GGDKE-TYNNIIRSGEKICRRPQEITRLQ-CRAKSHPEVSIEHLGQVVQCSREEGL---- 570

Qy         54 PVYTSTQEDCINSCCSTKNISGD-KACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAK 112
                        |  ::  |  | |  : :: |          :  |   : ||:
Db        571 ------------VCRNQDQQGPFKMC--LNYEVR---------VLCCETPKGCPVTSTS 606

Qy        113 GLMSYRIITDFPSLTRNLPSQELPQEDSLLHGQFSQ------------AVTPLAHHHTDY 160
                    :: : |: |::  | :  :  :|:    :              : || :  |
Db        607 VTAPSPLVGEPPAQTQSTSSWQKSRTTTLVTSSITSTTQTSTTSAPTTSTTPASIPSTTS 666

Qy        161 SKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLP 220
              :  |  :   | |                  ||   :      : :|   :   :
Db        667 APTTSTTSAPTTS---------------TTSAPTTSTTSTPQTTTSSAPTSSTTSAPTT 710

Qy        221 ENVSALPATVAVASP--HTTSATPKPATLLPTNASVTP----------SGTSQPQLATTA 268
                :|| | |  :::|   ||||      |  ||: |  |          | || |  :| :
Db        711 STISA-PTTSTISAPTTSTTSAPTASTTSAPTSTSSAPTTNTTSAPTTSTTSAPITSTIS 769

Qy        269 PPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNL 328
              | |: || | |: ||:  |     | |   |::  |:|  ||| |  |   |    |
Db        770 APTTSTTSTPQTSTISSPTTSTTPTPQTSTTSSPTTSTTSAPTTSTTSAPTTSTTSTPQT 829

Qy        329 TLNTGNVYNPT-ALSMSNVESSTMNKTASWEGREASPGSSSQGSVPE 374
              ::::    : | | : | : : |:      || :||  | |:
Db        830 SISSAPTSSTTSAPTASTISAPTTSTTSFHTTSTTSPPTSSTSSTPQ 876


RESULT 11
Q7YTR7
ID   Q7YTR7      PRELIMINARY;      PRT;   519 AA.
AC   Q7YTR7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein C30H6.11.
GN   ORFNames=C30H6.11;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Mortimore B.J.;
RL   Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z81044; CAE17706.1; -.
DR   WormBase; WBGene00007828; C30H6.11.
DR   WormPep; C30H6.11; CE34720.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   SMART; SM00034; CLECT; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   519 AA;  56012 MW;  93C2CFF9EC339D1A CRC64;

  Query Match             7.6%;  Score 168;  DB 2;  Length 519;
  Best Local Similarity   27.1%;  Pred. No. 0.0087;
  Matches   58;  Conservative   22;  Mismatches   96;  Indels   38;  Gaps    7;

Qy        229 TVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFT 288
              |    :| ||: ||   |  ||  : ||: |:     ||  | || |:   ||   | |
Db        155 TTTTTPTTTTTPTTTTTPTTTTTPTTTTTPTTTTTPTTTTAPTTTTTPTTTTTPTTTT 214

Qy        289 RAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVES 348
                  |     ||   |||    | :  :  | | |      | : || ||       ||
Db        215 TVPTTTTTTPTTTTTTTTTPTTTTTPTTTTTPAT-----TTSVGNNYNDANYYNSNHNE 269

Qy        349 -----STMNKTASWEGREASPGSSSQGSVPEN----QYGLPFE---KWLLIGSL------ 390
                  :  |  | ::       :|:  :  ||       ||       : |: |:
Db        270 AYNYYNYTNDNAHYD------NNSNNHNYSENFMRLMLSLPIAFSINFTLLNSIYLQHMK 323

Qy        391 --LFGVLFLVIGLVLLGRILSESLRRKRYSRLDY 422
                |  :||  :| | |       | || :  : |
Db        324 YDLTSILFNALGTVTL-------LMRKIFCNIQY 350


RESULT 12
Q685J2
ID   Q685J2      PRELIMINARY;      PRT;  4262 AA.
AC   Q685J2;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Secreted mucin MUC17.
GN   Name=MUC17;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreatic adenocarcinoma;
RA   Moniaux N., Andrianifahanana M., Jones A.M., Juntker W.M.,
RA   Schmied B.M., Batra S.K.;
RT   "Membrane-Anchored Mucin Expression in Pancreatic Adenocarcinoma:
RT   Characterization of a New Marker, MUC17.";
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreatic adenocarcinoma;
RA   Moniaux N.B.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ606308; CAE54436.1; -.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR011047; Quin_alc_DH_like.
DR   InterPro; IPR000082; SEA.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS50024; SEA; 1.
SQ   SEQUENCE   4262 AA;  425530 MW;  180AF264C8614284 CRC64;

  Query Match             7.4%;  Score 163;  DB 2;  Length 4262;
  Best Local Similarity   22.7%;  Pred. No. 0.26;
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  Matches   95;  Conservative   70;  Mismatches  161;  Indels   92;  Gaps   19;

Qy         16 ICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTS----TQEDCINSCCS-- 69
              :| ||| ||             ::  |::  :|:  |  |:      :| | :|  |
Db          9 LCLLTLVLS------------LLPPQAAAEQGLSVNRAVWDGGGCISQGDVLNRQCQQL 55

Qy         70 TKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP--SLT 127
              ::::    | |      |     :|  ||        :|   |    :   : :| |  | |
Db         56 SQHVRTGSATNTATGTTSTNVVEPRMYL-------SCSTNPEMTSIESSVTSDTPGVSST 108

Qy        128 RNLPSQELPQEDS------LLHGQFSQAVTPLAHHHTD--YSKPTDISWRDTLSQKFGSS 179
              |  |::     :|      |          :|     ||   | |::  |    |::  | |:
Db        109 RMTPTESRTTSESTSDSTTLFPSPTEDTSSPTTPEGTDVPMSTPSEESISSTMA--FVST 166

Qy        180 DHLEKL-------FKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAV 232
                 |          :|:|  |  |    :   | ::  |:       :|:: ::  :|
Db        167 APLPSFEAYTSLTYKVD-MSTPLTTSTQASSSPTTPEST------TIPKSTNSEGSTPLT 219

Qy        233 ASPHTTS--ATPKPATLLPT-----------NASVTPSGTSQPQLATTAPP--VTTVTS 276
              : | :|   |: :  ||| |             || :|:    | |: :||    | :|
Db        220 SMPASTMKVASSEAITLLTTPVEISTPVTISAQASSSPTTAEGPSLSNSAPSGGSTPLTR 279

Qy        277 QPPTTLI------STVFTRAAATLQAMATTAVLTTTFQAPTDSKG-SLETIPFTEISNLT 329
              | : ::      ||: |  |||   : |:   |    :|| ::| |: |  :|| |
Db        280 MPLSVMLVVSSEASTLSTTPAATNIPVITS---TEASSSPTTAEGTSIPTSTYTEGSTPL 336

Qy        330 LNTGNVYNPTA------LSMSNVESSTMNKTA--------SWEGREASPGSSSQGSVP 373
               :|     | |       ||:: |::||:  |:        : |       : |:|| |
Db        337 TSTPASTMPVATSEMSTLSITPVDTSTLVTTSTEPSSLPTTAEATSMLTSTLSEGSTP 394


RESULT 13
Q685J3
ID   Q685J3      PRELIMINARY;      PRT;  4493 AA.
AC   Q685J3;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Membrane mucin MUC17.
GN   Name=MUC17;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Moniaux N., Andrianifahanana M., Jones A.M., Juntker W.M.,
RA   Schmied B.M., Batra S.K.;
RT   "Membrane-Anchored Mucin Expression in Pancreatic Adenocarcinoma:
RT   Characterization of a New Marker, MUC17.";
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Moniaux N.B.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ606307; CAE54435.1; -.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR011047; Quin_alc_DH_like.
DR   InterPro; IPR000082; SEA.
DR   Pfam; PF01390; SEA; 1.
DR   SMART; SM00200; SEA; 1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS50024; SEA; 1.
SQ   SEQUENCE   4493 AA;  451718 MW;  06B1D6C680499AA5 CRC64;

  Query Match             7.4%;  Score 163;  DB 2;  Length 4493;
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              :| ||| ||             ::  |::  :|:  |  |:      :| | :|  |
Db          9 LCLLTLVLS------------LLPPQAAAEQGLSVNRAVWDGGGCISQGDVLNRQCQQL 55

Qy         70 TKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP--SLT 127
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Db         56 SQHVRTGSATNTATGTTSTNVVEPRMYL-------SCSTNPEMTSIESSVTSDTPGVSST 108

Qy        128 RNLPSQELPQEDS------LLHGQFSQAVTPLAHHHTD--YSKPTDISWRDTLSQKFGSS 179
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Db        109 RMTPTESRTTSESTSDSTTLFPSPTEDTSSPTTPEGTDVPMSTPSEESISSTMA--FVST 166

Qy        180 DHLEKL-------FKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAV 232
                 |          :|:|  |  |    :   | ::  |:       :|:: ::  :|
Db        167 APLPSFEAYTSLTYKVD-MSTPLTTSTQASSSPTTPEST------TIPKSTNSEGSTPLT 219

Qy        233 ASPHTTS--ATPKPATLLPT-----------NASVTPSGTSQPQLATTAPP--VTTVTS 276
              : | :|   |: :  ||| |             || :|:    | |: :||    | :|
Db        220 SMPASTMKVASSEAITLLTTPVEISTPVTISAQASSSPTTAEGPSLSNSAPSGGSTPLTR 279

Qy        277 QPPTTLI------STVFTRAAATLQAMATTAVLTTTFQAPTDSKG-SLETIPFTEISNLT 329
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Db        280 MPLSVMLVVSSEASTLSTTPAATNIPVITS---TEASSSPTTAEGTSIPTSTYTEGSTPL 336

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RESULT 14
Q14887
ID   Q14887      PRELIMINARY;      PRT;  477 AA.
AC   Q14887;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Mucin (Fragment).
GN   Name=MUC5AC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tracheobronchial mucosa;
RA   Guyonnet-Duperat V., Audie J., Debailleul V., Laine A., Buisine M.,
RA   Zouitina-Galiegue S., Pigny P., Aubert J., Porchet N.;
RT   "Characterization of the human mucin gene MUC5AC: a consensus
RT   cysteine-rich domain for 11p15 mucin genes.";
RL   Biochem. J. 0:0-0(1994).
DR   EMBL; Z34277; CAA84031.1; -.
DR   PIR; S53362; S53362.
FT   NON_TER       1      1
FT   NON_TER     477    477
SQ   SEQUENCE   477 AA;  50666 MW;  E7360031B4A51311 CRC64;

  Query Match             7.3%;  Score 160.5;  DB 2;  Length 477;
  Best Local Similarity   24.4%;  Pred. No. 0.024;
  Matches   66;  Conservative   42;  Mismatches  114;  Indels   49;  Gaps    9;

Qy        147 SQAVTPLAHHHTDYSKPTDISW---------RDTLSQKFGSSDHL----EKLFKMD---- 189
              || ||    |    ::|  |: :          ::| :    | : :    |:: ::
Db         15 SQPVTRDCHLRCTWTKWFDVDFPSPGPHGGDKETYNNIIRSGEKICRRPEEITRLQCRAE 74

Qy        190 ---EASAQLLAY-----KEKG-----HSQSSQFSS--DQEIAHLLPENVSALPATVAVAS 234
                 | | : |       :|:|      |    |    : |:  |  |     | |   ::
Db         75 SHPEVSIEHLGQVVQCSREEGLVCRNQDQQGPFKMCLNYEVRVLCCETPKGCPVT---ST 131

Qy        235 PHTTSATPKPATLLPTNAS----------VTPSGTSQPQLATTAPPVTTVTSQPPTTLI 283
              | |  :||      || ::          || | || || :||: | |: || | |:
Db        132 PVTAPSTPSGRATSPTQSTSSWQKSRTTTLVTTSTTSTPQTSTTSAPTTSTTSAPTTSTT 191

Qy        284 STVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLET---IPFTEISNLTLNTGNVYNPTA 340
              |   |   :| |   ::|  ::|  ||| |  |  |  |     |  :  |  :: |
Db        192 SAPTTSTTSTPQTSISSAPTSSTTSAPTSSTISARTTSIISAPTTSTTSFPTTSTTSATT 251
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Qy        341 LSMSNVESSTMNKTASWEGREASPGSSSQGS 371
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Db        252 TSTTSAPTSSTTSTPQTSKTSAATSSTTSGS 282


RESULT 15
Q8WWQ5
ID   Q8WWQ5      PRELIMINARY;      PRT;  2448 AA.
AC   Q8WWQ5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mucin 5 (Fragment).
GN   Name=MUC5AC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Trachea;
RX   MEDLINE=21426417; PubMed=11535137; DOI=10.1042/0264-6021:3580763;
RA   Escande F., Aubert J.P., Porchet N., Buisine M.P.;
RT   "Human mucin gene MUC5AC: organization of its 5'-region and central
RT   repetitive region.";
RL   Biochem. J. 358:763-772(2001).
DR   EMBL; AJ298317; CAC83674.1; -.
DR   HSSP; P56682; 1CCV.
DR   Genew; HGNC:7515; MUC5AC.
DR   Pfam; PF01826; TIL; 2.
DR   Pfam; PF00094; VWD; 3.
DR   SMART; SM00214; VWC; 3.
DR   SMART; SM00216; VWD; 3.
DR   PROSITE; PS00527; RIBOSOMAL_S14; UNKNOWN_2.
FT   NON_TER    2448   2448
SQ   SEQUENCE   2448 AA;  260968 MW;  A5C1BD627844D952 CRC64;

  Query Match             7.1%;  Score 157.5;  DB 2;  Length 2448;
  Best Local Similarity   23.1%;  Pred. No. 0.29;
  Matches   87;  Conservative   38;  Mismatches  142;  Indels  109;  Gaps   16;

Qy         63 CIN-----SCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSY 117
              | |      || | |:             |   | |      |         |
Db       2034 CYNYEIRIQCCETVNV-----------CRDITRPPKTVATTRPTPH-----PTGAQTQT 2076

Qy        118 RIITDFPSLTRNLP---SQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISW------ 168
                |  || :   |   |:  |   |:  |  :  ||   |    ::   |: :
Db       2077 TFTTHMPSASTEQPTATSRGGPTATSVTQGTHTTPVTRNCHPRCTWTTWFDVDFPSPGPH 2136

Qy        169 ---RDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSS--------QFSSDQ---- 213
                 ::| :    |    ||: :  |   :|  : | | : |        | | ::
Db       2137 GGDKETYNNIIRSG---EKICRRPEEITRLQC-RAKSHPEVSIEHLGQVVQCSREEGLVC 2192

Qy        214 --------------EIAHLLPENVSALPATVAVASPHTTSATPKPATLLPTNAS----- 253
                          |:  |  |     | |   ::| |  :||    : || ::
Db       2193 RNQDQQGPFKMCLNIEVRVLCCETPKGCPVT---STPVTAPSTPSGRAISPTQSTSSWQK 2249

Qy        254 ------VTPSGTSQPQLATT---------AP-------PVTTVTSQPPTTLISTVFTRAA 291
                   || | || || :||          ||       | |: || | |: ||   |  :
Db       2250 SRTTTLVTTSTTSTPQTSTTYAHTTSTTSAPTARTTSAPTTSTTSVPTTSTISGPKTTPS 2309

Qy        292 ATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTM 351
                  |:|  |:|  ||| |  |   :| |  | : | |     ||          |
Db       2310 PVPTTSTTSAATTSTISAPTTSTTS---VPGTTPSPV-LTTSTTSAPT----------TR 2355

Qy        352 NKTASWEGREASPGSS 367
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Db       2356 TTSASPAGTTSGPGNT 2371


Search completed: April 26, 2005, 21:51:30
Job time : 128 secs
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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 26, 2005, 21:59:56 ; Search time 4716 Seconds
(without alignments)
4428.371 Million cell updates/sec

Title: US-10-735-014-83
Perfect score: 2211
Sequence: 1 MFFGGEGSLTYTLVIICFLT.....LRRKRYSRLDYLINGIYVDI 431

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	2211	100.0	2284	6	AR252736	AR252736 Sequence
3	2211	100.0	2284	6	AR429104	AR429104 Sequence
4	2211	100.0	2284	6	AR534995	AR534995 Sequence
5	2211	100.0	2284	6	AX403627	AX403627 Sequence
6	2211	100.0	2284	9	AY358563	AY358563 Homo sapi
7	2211	100.0	2297	6	BD160088	BD160088 Primer fo
8	2211	100.0	2297	6	AX883044	AX883044 Sequence
9	2211	100.0	2297	9	AK023622	AK023622 Homo sapi
10	2210	100.0	2333	9	BC032998	BC032998 Homo sapi
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12	2039	92.2	2345	9	AB060888	AB060888 Macaca fa
13	2022	91.5	2221	6	BD155963	BD155963 Primer fo
14	2022	91.5	2221	6	CQ776818	CQ776818 Sequence
15	2022	91.5	2221	6	AX876122	AX876122 Sequence
16	2022	91.5	2221	9	AK001160	AK001160 Homo sapi
c 17	1573.5	71.2	144000	9	AC007621	AC007621 Homo sapi
c 18	1573.5	71.2	188344	2	AC131617	AC131617 Homo sapi
19	1216	55.0	735	6	CQ735543	CQ735543 Sequence
20	1179.5	53.3	2288	10	BC039930	BC039930 Mus muscu
21	1164.5	52.7	2286	6	CQ777667	CQ777667 Sequence
22	835	37.8	548	6	BD059530	BD059530 Secreted
23	780.5	35.3	805	6	BD149896	BD149896 Primer fo
24	780.5	35.3	805	6	AX869834	AX869834 Sequence
25	764.5	34.6	855	6	BD147198	BD147198 Primer fo
26	764.5	34.6	855	6	AX867136	AX867136 Sequence
27	709.5	32.1	110134	2	AC149660	AC149660 Bos tauru
c 28	683.5	30.9	224870	2	AC129657	AC129657 Rattus no
c 29	683.5	30.9	250782	2	AC128093	AC128093 Rattus no
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31	678	30.7	236589	2	AC118035	AC118035 Mus muscu
32	633	28.6	422	6	BD071236	BD071236 Secreted
33	522	23.6	1627	5	AJ719946	AJ719946 Gallus ga
34	503	22.7	1326	10	BC031372	BC031372 Mus muscu
35	386	17.5	188344	2	AC131617	AC131617 Homo sapi
36	338.5	15.3	242590	2	AC133722	AC133722 Rattus no
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38	242	10.9	295	6	AX894034	AX894034 Sequence
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ALIGNMENTS

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LOCUS BD140585 2284 bp DNA linear PAT 18-SEP-2002
DEFINITION Polypeptides and nucleic acids encoding the same.
ACCESSION BD140585
VERSION BD140585.1 GI:23235530
KEYWORDS JP 2002505850-A/68.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2284)
AUTHORS Wood,W.I., Goddard,A., Gurney,A.L., Yuan,J., Baker,K.P. and
Zheng,J.
TITLE Polypeptides and nucleic acids encoding the same
JOURNAL Patent: JP 2002505850-A 68 26-FEB-2002;
GENENTECH INC
COMMENT OS Homo sapiens (human)
PN JP 2002505850-A/68
PD 26-FEB-2002
PF 01-DEC-1998 JP 2000523338
PR 03-DEC-1997 US 60/067411,11-DEC-1997 US 60/069334 PR
11-DEC-1997 US 60/069335,11-DEC-1997 US 60/069278 PR
12-DEC-1997 US 60/069425,16-DEC-1997 US 60/069696 PR
16-DEC-1997 US 60/069694,16-DEC-1997 US 60/069702 PR
17-DEC-1997 US 60/069870,17-DEC-1997 US 60/069873 PR
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09-FEB-1998 US 60/074086,09-FEB-1998 US 60/074092 PR

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            25-FEB-1998 US    60/075945
            PI   WILLIAM I WOOD,AUDREY GODDARD,AUSTIN L GURNEY,JEAN YUAN,KEVIN
            PI   P BAKER,
            PI   JIAN ZHENG
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12P21/02,
            PC   C12P21/08,C12Q1/68,C12N15/00,C12N5/00
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                     /mol_type="genomic DNA"
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ORIGIN

Alignment Scores:
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Score:                  2211.00         Matches:        431
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-735-014-83 (1-431) x BD140585 (1-2284)

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Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 2
AR252736
LOCUS       AR252736                2284 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 514 from patent US 6478825.
ACCESSION   AR252736
VERSION     AR252736.1  GI:27300644
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2284)
  AUTHORS   Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
  TITLE     Implant, method of making same and use of the implant for the
            treatment of bone defects
  JOURNAL   Patent: US 6478825-A 514 12-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .2284
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              5.79e-112       Length:         2284
Score:                  2211.00         Matches:        431
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-735-014-83 (1-431) x AR252736 (1-2284)
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Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518
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RESULT 3
AR429104

LOCUS	AR429104	2284 bp DNA	linear PAT 18-DEC-2003
DEFINITION	Sequence 82 from patent US 6642360.		
ACCESSION	AR429104		
VERSION	AR429104.1 GI:40189199		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
	Unclassified.		
REFERENCE	1 (bases 1 to 2284)		
AUTHORS	Filvaroff,E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L. and Wood,W.I.		
TITLE	Secreted polypeptides that stimulate release of proteoglycans from cartilage		
JOURNAL	Patent: US 6642360-A 82 04-NOV-2003;		

FEATURES	Location/Qualifiers
source	1. .2284
	/organism="unknown"
	/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.:	5.79e-112	Length:	2284
Score:	2211.00	Matches:	431
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-735-014-83 (1-431) x AR429104 (1-2284)

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Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

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Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
                |||||||||||||||||||||||||||||||
Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 4
AR534995
LOCUS       AR534995               2284 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 82 from patent US 6734288.
ACCESSION   AR534995
VERSION     AR534995.1  GI:53925785
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.

REFERENCE   1  (bases 1 to 2284)
  AUTHORS   Filvaroff,E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L.
            and Wood,W.I.
  TITLE     Antibodies against a secreted polypeptide that stimulates release
            of proteoglycans from cartilage
  JOURNAL   Patent: US 6734288-A 82 11-MAY-2004;
FEATURES             Location/Qualifiers
     source          1. .2284
                     /organism="unknown"
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ORIGIN

Alignment Scores:
Pred. No.:                5.79e-112       Length:          2284
Score:                    2211.00         Matches:         431
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       6               Gaps:            0

US-10-735-014-83 (1-431) x AR534995 (1-2284)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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LOCUS       AX403627               2284 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 514 from Patent WO0073454.
ACCESSION   AX403627
VERSION     AX403627.1  GI:21437090
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
            Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
            Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
            Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Williams,P., Wood,W.I. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
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  JOURNAL   Patent: WO 0073454-A 514 07-DEC-2000;
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ORIGIN
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US-10-735-014-83 (1-431) x AX403627 (1-2284)

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ACCESSION   AY358563
VERSION     AY358563.1  GI:37182247
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REFERENCE   1  (bases 1 to 2284)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
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            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 2284)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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US-10-735-014-83 (1-431) x AY358563 (1-2284)

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Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 7
BD160088
LOCUS       BD160088                2297 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD160088
VERSION     BD160088.1  GI:27865846
KEYWORDS    JP 2002191363-A/14931.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2297)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 14931 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002191363-A/14931
            PD   09-JUL-2002
            PF   28-JUL-2000 JP 2000280990
            PI   TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
            PI   SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
             Primer for synthesizing full-length cDNA and use thereof FH   Key
                    Location/Qualifiers
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FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
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Score:                  2211.00         Matches:        431
Percent Similarity:     100.00%         Conservative:   0
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US-10-735-014-83 (1-431) x BD160088 (1-2297)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Db        259 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 318

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Db        319 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 378

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        439 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 498

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Db        499 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 558

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Db        979 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1038

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Db       1099 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1158

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Db       1159 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1218

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Db       1219 CCGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1278

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Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Db       1399 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1458

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1459 CTCGTCCTCCTGGGTAGAATCCTCTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1518

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db       1519 GATTATTTGATCAATGGGATCTATGTGGACATC 1551

RESULT 8
AX883044
LOCUS       AX883044               2297 bp    DNA     linear   PAT 17-DEC-2003
DEFINITION  Sequence 17949 from Patent EP1074617.
ACCESSION   AX883044
VERSION     AX883044.1  GI:40037945
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primers for synthesising full-length cDNA and their use
  JOURNAL   Patent: EP 1074617-A 17949 07-FEB-2001;
            Research Association for Biotechnology (JP)
FEATURES             Location/Qualifiers
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                     QPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGN
                     VYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSVPENQYGLPFEKWLLIGSLLF
                     GVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI"
ORIGIN

Alignment Scores:
Pred. No.:          5.82e-112      Length:         2297
Score:              2211.00        Matches:        431
Percent Similarity: 100.00%        Conservative:   0
Best Local Similarity: 100.00%     Mismatches:     0
Query Match:        100.00%        Indels:         0
DB:                 6              Gaps:           0

US-10-735-014-83 (1-431) x AX883044 (1-2297)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Db        259 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 318

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Db        319 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 378

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Db        379 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 438

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        439 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 498

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        499 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 558

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Db        559 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 618

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 678

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 738

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Db        739 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 798

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        859 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 918

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        919 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 978

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Db        979 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1038

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Db       1039 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1098

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db       1159 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1218

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Db       1219 CCGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1278

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Db       1279 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1338

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db       1519 GATTATTTGATCAATGGGATCTATGTGGACATC 1551

RESULT 9
AK023622
LOCUS       AK023622               2297 bp    mRNA    linear   PRI 30-JAN-2004
DEFINITION  Homo sapiens cDNA FLJ13560 fis, clone PLACE1007877.
ACCESSION   AK023622
VERSION     AK023622.1  GI:10435603
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,
            Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
            Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
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            Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J.,
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            Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
  TITLE     Complete sequencing and characterization of 21,243 full-length
            human cDNAs
  JOURNAL   Nat. Genet. 36 (1), 40-45 (2004)
   PUBMED   14702039
REFERENCE   2
  AUTHORS   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
            Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
            Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
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            Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
            Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
            Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 2297)
  AUTHORS   Isogai,T. and Otsuki,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            International Trade and Industry of Japan; cDNA full insert
            sequencing: Research Association for Biotechnology; cDNA library
            construction, 5'- & 3'-end one pass sequencing and clone selection:
            Helix Research Institute (supported by Japan Key Technology Center
            etc.) and Department of Virology, Institute of Medical Science,
            University of Tokyo.

FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:                5.82e-112       Length:          2297
Score:                    2211.00         Matches:         431
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       9               Gaps:            0

US-10-735-014-83 (1-431) x AK023622 (1-2297)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Db        259 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 318

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Db        319 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 378

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Db        379 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 438

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        439 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 498

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        499 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 558

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Db        559 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 618

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Db        619 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 678

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        679 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 738

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Db        739 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 798

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Db        799 CACTTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 858
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Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        859 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 918

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db       1099 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1158

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Db       1339 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1398

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1459 CTCGTCCTCCTGGGTAGAATCCTCTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1518

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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RESULT 10
BC032998

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LOCUS       BC032998               2333 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens MANSC domain containing 1, mRNA (cDNA clone MGC:26021
            IMAGE:4824116), complete cds.
ACCESSION   BC032998
VERSION     BC032998.2  GI:34189992
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2333)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 2333)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     On Aug 25, 2003 this sequence version replaced gi:21542502.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI) &  Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 33 Row: h Column: 14
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 8922334.
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                     VYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSVPENQYGLPFEKWLLIGSLLF
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ORIGIN
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Pred. No.:                6.72e-112       Length:          2333
Score:                    2210.00         Matches:         430
Percent Similarity:       100.00%         Conservative:    1
Best Local Similarity:    99.77%          Mismatches:      0
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Query Match:          99.95%      Indels:        0
DB:                   9           Gaps:          0

US-10-735-014-83 (1-431) x BC032998 (1-2333)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Db        276 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 335

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Db        336 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 395

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        456 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 515

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        516 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 575

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Db        636 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 695

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        696 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 755

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Db        756 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 815

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        936 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 995

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Db        996 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1055

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Db       1056 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1115

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db       1116 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1175

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db       1176 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1235

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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Db       1416 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTTTTTGGTGTCCTGTTCCTGGTGATAGGC 1475

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1476 CTCGTCCTCCTGGGTAGAATCCTCTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1535

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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RESULT 11
BD227259
LOCUS       BD227259               2015 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Secreted proteins and polynucleotides encoding them.
ACCESSION   BD227259
VERSION     BD227259.1  GI:33037029
KEYWORDS    JP 2002522062-A/20.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2015)
  AUTHORS   Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A.C., Evans,C.,
            Merberg,D., Treacy,M., Agostino,M.J., Ii,R.J.S., Spaulding,V.,
            Wong,G.G., Clark,H.F. and Fechtel,K.
  TITLE     Secreted proteins and polynucleotides encoding them
  JOURNAL   Patent: JP 2002522062-A 20 23-JUL-2002;
            GENETICS INSTITUTE INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002522062-A/20
            PD   23-JUL-2002
            PF   13-AUG-1999 JP 2000565001
            PR   14-AUG-1998 US    60/096622,17-AUG-1998 US    60/096815 PR
            04-SEP-1998 US    60/099229,23-OCT-1998 US    60/105368 PR
            08-JAN-1999 US    60/115234,12-FEB-1999 US    60/119931 PR
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            11-AUG-1999 US    60/148424
            PI   KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A COLLINS
            PI   RACIE,
            PI   CHERYL EVANS,DAVID MERBERG,MAURICE TREACY,MICHAEL J AGOSTINO,
            PI   ROBERT J STEININGER II,VIKKI SPAULDING,GORDON G WONG,HILARY F
            PI   CLARK,
            PI   KIM FECHTEL
            PC   C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61K48/00,
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            PC   A61P7/02,A61P7/04,A61P7/06,A61P13/00,A61P29/00,A61P35/00, PC
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            PC   A61P43/00,A61P43/00,C07K14/47,C12N5/10,C12P21/02,G01N33/15, PC
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            PC   C12N15/00,C12N5/00,A61K37/02
            CC   Secreted proteins and polynucleotides encoding them FH   Key
                      Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
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ORIGIN

Alignment Scores:
Pred. No.:              6.95e-104       Length:         2015
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Best Local Similarity: 99.51%        Mismatches:    1
Query Match:           93.26%        Indels:        2
DB:                    6             Gaps:          0

US-10-735-014-83 (1-431) x BD227259 (1-2015)

Qy         22 ArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAspIle 41
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATC 60

Qy         42 GlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGlnGlu 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAAGAA 120

Qy         62 AspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsnLeu 81
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAACTTG 180

Qy         82 MetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCysPro 101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGTCCC 240

Qy        102 AsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIleThr 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATTACA 300

Qy        122 AspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSerLeu 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCTCTC 360

Qy        142 LeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyrSer 161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTATTCA 420

Qy        162 LysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAspHis 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGATCAC 480

Qy        182 LeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGluLys 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAAAAA 540

Qy        202 GlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuProGlu 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCTGAA 600

Qy        222 AsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAlaThr 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCTACT 660

Qy        242 ProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSerGln 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCCCAG 720

Qy        262 ProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThrThr 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACGACC 780

Qy        282 LeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThrAla 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACAGCA 840

Qy        302 ValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIlePro 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATACCG 900

Qy        322 PheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAlaLeu 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCACTT 960

Qy        342 SerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArgGlu 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGGGAG 1020

Qy        362 AlaSerProGlySerSerSer-GlnGlySerValProGluAsnGlnTyrGlyLeuProPh 381
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1021 GCCAGTCCAGGCAGTTCCTCCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCATT 1080

Qy        381 eGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGlyLe 401
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGCCT 1140

Qy        401 uValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeuAs 421
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1141 CGTCCTCCTGGGTAGATC-CTCTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGA 1199

Qy        421 pTyrLeuIleAsnGlyIleTyrValAspIle 431
              |||||||||||||||||||||||||||||||
Db       1200 TTATTTGATCAATGGGATCTATGTGGACATC 1230
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RESULT 12
AB060888

```
LOCUS       AB060888               2345 bp    mRNA    linear   PRI 13-JUN-2001
DEFINITION  Macaca fascicularis brain cDNA clone:QtrA-13483, full insert
            sequence.
ACCESSION   AB060888
VERSION     AB060888.1  GI:13874554
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Macaca fascicularis (crab-eating macaque)
  ORGANISM  Macaca fascicularis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (sites)
  AUTHORS   Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
            Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
  TITLE     Isolation of full-length cDNA clones from macaque brain cDNA
            libraries
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2345)
  AUTHORS   Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-APR-2001) Katsuyuki Hashimoto, National Institute of
            Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
            1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
            (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/,
            Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
COMMENT     Lab host:    TOP10
            Vector:      pME18S-FL3 (Acc.No. AB009864)
            R.  Site1:   DraIII (CACTGTGTG)
            R.  Site2:   DraIII (CACCATGTG)
            Description: 1st strand cDNA was primed with an oligo(dT) primer
            [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized
            using specific 5' and 3' primers and amplified by PCR.  The PCR
            product was digested with SfiI and size selection was performed to
            exclude fragments <1.5kb.The SfiI-digested PCR product was cloned
            into distinct DraIII sites of pME18S-FL3. XhoI sites just outside
            the DraIII sites can be used to isolate the cDNA insert.  Libraries
            were constructed by oligo-capping method
            (Sugano et al., , Institute of Medical Science, University of
            Tokyo).
            Custom primer used for sequencing
            ( 5' end primer [CTTCTGCTCTAAAAGCTGCG];
            3' end primer [CGACCTGCAGCTCGAGCACA] ).
FEATURES             Location/Qualifiers
     source          1. .2345
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                     /mol_type="mRNA"
                     /db_xref="taxon:9541"
                     /clone="QtrA-13483"
                     /sex="male"
                     /tissue_type="temporal lobe right"
                     /clone_lib="macaque brain cDNA library QtrA"
                     /dev_stage="adult"
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                     /codon_start=1
                     /product="hypothetical protein"
                     /protein_id="BAB46892.1"
                     /db_xref="GI:13874555"
                     /translation="MFFGGKGSLTYTLVIICFLTLRLAASQNCLNKSLEDVVIDIQSS
                     LSKGIRGNEPIYTSTQEDCINSCCSTKIISGDKACNFMIFDTRKIARRPNCYLFFCPN
                     EEACPLKPAKGLRSYRIIRDFPSLTRNLPSQELPQEDSLLPGQFSQAVTPLARHHIVY
                     SKPTDISWRETLPQKFGSSDHLEKLFNMDKASAQLLVYKEKGHSQSSQISSDQEIAHL
                     LPENVSVFPATVAVASPHTTSATPKPAIRLPTNASVTPSGTSQPQLATTSPPVTTVTS
                     QPPTTLISTGFTRAVATLQAMATTAVLTTTFQAPTDLKGSLETIPFTEISNLTLNTGN
                     VYNPTALSMSNVKSSATNKTASWEGREASPGRSSQGNVPENQYGLPFEKWLLIGSLLF
                     GVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI"
ORIGIN

Alignment Scores:
Pred. No.:                1.5e-102        Length:          2345
Score:                    2039.00         Matches:         398
Percent Similarity:       94.43%          Conservative:    9
Best Local Similarity:    92.34%          Mismatches:      24
Query Match:              92.22%          Indels:          0
DB:                       9               Gaps:            0

US-10-735-014-83 (1-431) x AB060888 (1-2345)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              |||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||
Db        255 ATGTTCTTTGGGGGAAAAGGGAGCTTGACCTACACTTTGGTAATAATTTGCTTCCTGACA 314

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
              |||||||||:::|||||||||||||||||||   |||||||||||||||||||||||||||
Db        315 CTAAGGCTGGCTGCTAGTCAGAATTGCCTCAACAAGAGTCTAGAAGATGTTGTCATTGAC 374

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              |||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        375 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCATATATACTTCAACTCAA 434

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              |||||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db        435 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAATCATATCAGGGGACAAAGCATGTAAC 494

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              |||||||||||||||||||||||   ||||||:::|||||||||||||||||||||||||
Db        495 TTCATGATCTTCGACACTCGAAAAATAGCCAGACGACCCAACTGCTACCTATTTTTCTGT 554

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              |||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        555 CCCAATGAGGAAGCCTGTCCACTGAAACCAGCAAAAGGACTTAGGAGTTACAGGATAATT 614

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        615 AGAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAGGACTCT 674

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||   |||||||||||||||||||||||||||||||||   |||||      |||
Db        675 CTCTTACCTGGCCAGTTTTCACAAGCAGTCACTCCTCTAGCCCGTCATCACATAGTTTAT 734

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              |||||||||||||||||||||||||||:::||||||   ||||||||||||||||||||
Db        735 TCAAAGCCCACCGATATCTCATGGAGAGAGACACTTCCTCAGAAGTTTGGATCCTCAGAT 794

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              ||||||||||||||||   ||||||:::||||||||||||||||   |||||||||
Db        795 CACTTGGAGAAACTATTTAATATGGACAAAGCAAGTGCCCAGCTCCTTGTTTATAAAGAA 854

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        855 AAAGGCCATTCTCAGAGTTCACAGATTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 914

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
              ||||||||||||      ||||||||||||||||||||||||||||||||||||||||||
Db        915 GAAAATGTGAGTGTGTTCCCAGCTACAGTGGCAGTTGCCTCTCCACATACCACCTCGGCT 974

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        975 ACTCCAAAGCCCGCCATCCGTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1034

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db       1035 CAGCCACAGCTGGCCACCACATCTCCGCCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1094

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
              ||||||||||||||    ||||||||||||    ||||||||||||||||||||||||||
Db       1095 ACCCTCATTTCTACAGGTTTTACACGGGCTGTGGCTACACTCCAAGCAATGGCTACAACA 1154

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
              ||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db       1155 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTTGAAAGGCAGCCTAGAAACGATA 1214

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1215 CCGTTTACAGAAATCTCCAACCTCACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1274

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
              ||||||||||||||||||:::||||||    ||||||||||||||||||||||||||||||
Db       1275 CTTTCTATGTCAAATGTGAAGTCTTCCGCTACGAATAAAACTGCTTCCTGGGAAGGTAGG 1334

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
              ||||||||||||||    ||||||||||||:::||||||||||||||||||||||||||
Db       1335 GAGGCCAGTCCAGGTCGTTCCTCCCAGGGCAACGTTCCAGAAAATCAGTATGGCCTTCCA 1394

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1395 TTTGAAAAGTGGCTTCTTATCGGATCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1454

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1455 CTCGTCCTCCTGGGCAGAATCCTCTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1514

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
              |||||||||||||||||||||||||||||||||
Db       1515 GATTATTTGATCAATGGGATCTATGTGGACATC 1547

RESULT 13
BD155963
LOCUS       BD155963               2221 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD155963
VERSION     BD155963.1  GI:27861721
KEYWORDS    JP 2002191363-A/10806.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2221)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 10806 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002191363-A/10806
            PD   09-JUL-2002
            PF   28-JUL-2000 JP 2000280990
            PI   TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
            PI   SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
             Primer for synthesizing full-length cDNA and use thereof FH   Key
                       Location/Qualifiers
            FT   CDS             (266). .(1456).
FEATURES              Location/Qualifiers
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                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.19e-101       Length:         2221
Score:                  2022.00         Matches:        397
Percent Similarity:     92.11%          Conservative:   0
Best Local Similarity:  92.11%          Mismatches:     0
Query Match:            91.45%          Indels:         34
DB:                     6               Gaps:           1

US-10-735-014-83 (1-431) x BD155963 (1-2221)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              ||||||||||||||||||||||||||||||||||||||
Db        266 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTG---------------------- 304

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40

Db        304 ------------------------------------------------------------ 304

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
                                    ||||||||||||||||||||||||||||||||||||||
Db        305 --------------------GGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 343

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 403

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 463

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 523

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 583

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 643

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Db        644 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 703

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Db        704 CACTTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 763

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 823

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        824 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 883

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 943

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        944 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1003

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1063

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db       1064 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1123

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Db       1184 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1243

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Db       1244 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1303

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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Db       1304 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1363

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1364 CTCGTCCTCCTGGGTAGAATCCTCTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1423

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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RESULT 14
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LOCUS       CQ776818               2221 bp    DNA     linear   PAT 11-MAR-2004
DEFINITION  Sequence 504 from Patent EP1394274.
ACCESSION   CQ776818
VERSION     CQ776818.1  GI:45380208
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K.
  TITLE     Methods of testing for bronchial asthma or chronic obstructive
            pulmonary disease
  JOURNAL   Patent: EP 1394274-A 504 03-MAR-2004;
            Genox Research, Inc. (JP)
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              1.19e-101       Length:         2221
Score:                  2022.00         Matches:        397
Percent Similarity:     92.11%          Conservative:   0
Best Local Similarity:  92.11%          Mismatches:     0
Query Match:            91.45%          Indels:         34
DB:                     6               Gaps:           1

US-10-735-014-83 (1-431) x CQ776818 (1-2221)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Db        266 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTG---------------------- 304

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40

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Qy        41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Db       344 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 403

Qy        81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db       404 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 463

Qy       101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Db       464 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 523

Qy       121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Qy       301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db      1064 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1123

Qy       321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Db      1124 CCGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1183

Qy       341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Qy       401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db      1364 CTCGTCCTCCTGGGTAGAATCCTCTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1423

Qy       421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db      1424 GATTATTTGATCAATGGGATCTATGTGGACATC 1456

RESULT 15
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LOCUS       AX876122               2221 bp    DNA     linear   PAT 17-DEC-2003
DEFINITION  Sequence 11027 from Patent EP1074617.
ACCESSION   AX876122
VERSION     AX876122.1  GI:40030858
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primers for synthesising full-length cDNA and their use
  JOURNAL   Patent: EP 1074617-A 11027 07-FEB-2001;
            Research Association for Biotechnology (JP)
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ORIGIN

Alignment Scores:
Pred. No.:              1.19e-101      Length:          2221
Score:                  2022.00        Matches:         397
Percent Similarity:     92.11%         Conservative:    0
Best Local Similarity:  92.11%         Mismatches:      0
Query Match:            91.45%         Indels:          34
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US-10-735-014-83 (1-431) x AX876122 (1-2221)

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Qy        21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40

Db       304 ------------------------------------------------------------ 304

Qy        41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Db       344 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 403

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Db        524 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 583

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        584 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 643

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        764 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 823

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Db        944 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1003

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db       1184 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1243

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1304 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1363

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1364 CTCGTCCTCCTGGGTAGAATCCTCTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1423

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
              |||||||||||||||||||||||||||||||
Db       1424 GATTATTTGATCAATGGGATCTATGTGGACATC 1456
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Search completed: April 26, 2005, 23:55:03
Job time : 4743 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 26, 2005, 21:54:06 ; Search time 604 Seconds
(without alignments)
4224.186 Million cell updates/sec

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Perfect score: 2211
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	2211	100.0	2284	8	ABX80978	Abx80978 Human sec
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34	2211	100.0	2284	9	ADA39496	Ada39496 Human cDN
35	2211	100.0	2284	9	ADB96522	Adb96522 Human PRO
36	2211	100.0	2284	10	ADC57994	Adc57994 Human PRO
37	2211	100.0	2284	10	ADC25838	Adc25838 Human cDN
38	2211	100.0	2284	10	ADC25596	Adc25596 Human cDN
39	2211	100.0	2284	10	ADC55358	Adc55358 Human PRO
40	2211	100.0	2284	10	ADC12225	Adc12225 Human cDN
41	2211	100.0	2284	10	ADC56647	Adc56647 Human PRO
42	2211	100.0	2284	10	ADC11692	Adc11692 Human cDN
43	2211	100.0	2284	10	ADC25717	Adc25717 Human cDN
44	2211	100.0	2284	10	ADC14814	Adc14814 Novel hum
45	2211	100.0	2284	10	ADD08346	Add08346 Novel hum

ALIGNMENTS

RESULT 1
AAX80059
ID AAX80059 standard; cDNA; 2284 BP.
XX
AC AAX80059;
XX
DT 12-AUG-1999 (first entry)
XX
DE Human PRO361 nucleotide sequence.
XX
KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
KW secreted protein; transmembrane protein; inflammation disorder; ss.
XX
OS Homo sapiens.
XX
PN WO9928462-A2.
XX
PD 10-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US025108.
XX
PR 03-DEC-1997; 97US-0067411P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 16-DEC-1997; 97US-0069694P.
PR 16-DEC-1997; 97US-0069696P.
PR 16-DEC-1997; 97US-0069702P.

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PR   17-DEC-1997;   97US-0069870P.
PR   17-DEC-1997;   97US-0069873P.
PR   18-DEC-1997;   97US-0068017P.
PR   05-JAN-1998;   98US-0070440P.
PR   09-FEB-1998;   98US-0074086P.
PR   09-FEB-1998;   98US-0074092P.
PR   25-FEB-1998;   98US-0075945P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Wood WI,  Goddard A,  Gurney AL,  Yuan J,  Baker KP,  Chen J;
XX
DR   WPI; 1999-371118/31.
DR   P-PSDB; AAY17834.
XX
PT   Nucleic acids encoding PRO secreted and transmembrane proteins.
XX
PS   Claim 2; Fig 36; 123pp; English.
XX
CC   The present invention describes nucleic acids encoding PRO secreted and
CC   transmembrane proteins used therapeutically. The PRO proteins have
CC   cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
CC   activity. The proteins and polynucleotides can be used in therapy,
CC   identification of homologues, raising antibodies and design of probes and
CC   primers. They can be used in a range of diseases related to proteins that
CC   they have homology with, e.g. a PRO protein having homology to complement
CC   proteins may be used in inflammatory responses
XX
SQ   Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.02e-141       Length:         2284
Score:                  2211.00         Matches:        431
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     2               Gaps:           0

US-10-735-014-83 (1-431) x AAX80059 (1-2284)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
              |||||||||||||||||||||||||||||||||
Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 2
AAA49567
ID   AAA49567 standard; cDNA; 2284 BP.
XX
AC   AAA49567;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Human PRO361 cDNA.
XX
KW   PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243;
KW   PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347; PRO355; PRO353;
KW   PRO361; PRO365; transmembrane polypeptide; antibody; screening;
KW   detection; inhibition; probe; primer; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
```

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FT   CDS             226. .1521
FT                   /*tag= a
FT                   /product= "PRO361 polypeptide"
XX
PN   WO200032776-A2.
XX
PD   08-JUN-2000.
XX
PF   01-DEC-1999;   99WO-US028301.
XX
PR   01-DEC-1998;   98WO-US025108.
PR   16-DEC-1998;   98US-0112850P.
PR   22-DEC-1998;   98US-0113296P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Botstein D,  Eaton DL,  Ferrara N,  Filvaroff E;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Grimaldi CJ,  Gurney AL;
PI   Hillan KJ,  Kljavin IJ,  Napier MA,  Roy MA,  Tumas D,  Wood WI;
XX
DR   WPI; 2000-412324/35.
DR   P-PSDB; AAB01325.
XX
PT   New human nucleic acids encoding secreted and transmembrane polypeptides,
PT   designated as PRO polypeptides, useful as pharmaceutical and diagnostic
PT   agents.
XX
PS   Claim 2; Fig 31; 187pp; English.
XX
CC   New human nucleic acids encoding secreted and transmembrane polypeptides
CC   which are designated as PRO polypeptides are described The membrane-bound
CC   proteins have various industrial applications, including as
CC   pharmaceutical and diagnostic agents. The membrane-bound proteins can
CC   also be employed for screening of potential peptide or small molecule
CC   inhibitors of the relevant receptor/ligand interaction. Anti-PRO
CC   antibodies are useful for the affinity purification of PRO from
CC   recombinant cell culture or natural sources
XX
SQ   Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.02e-141      Length:          2284
Score:                    2211.00        Matches:         431
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       3              Gaps:            0

US-10-735-014-83 (1-431) x AAA49567 (1-2284)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
              |||||||||||||||||||||||||||||||||
Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 3
AAF44268
ID   AAF44268 standard; cDNA; 2284 BP.
XX
AC   AAF44268;
XX
DT   02-APR-2001  (first entry)
XX
```

DE Human PRO361 nucleotide sequence SEQ ID NO:514.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay; ss.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
DR P-PSDB; AAB65299.
XX
PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
PS Claim 2; Fig 327; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
SQ Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.02e-141	Length:	2284
Score:	2211.00	Matches:	431
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	5	Gaps:	0

US-10-735-014-83 (1-431) x AAF44268 (1-2284)

```
Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185
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Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
              |||||||||||||||||||||||||||||||
Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518
```

RESULT 4
ACA64519
ID ACA64519 standard; cDNA; 2284 BP.
XX
AC ACA64519;
XX
DT 17-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO361 cDNA.
XX
KW Human; secreted and transmembrane protein; cytostatic; anti-HIV;
KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
KW PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;
KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
KW drug screening; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003003531-A1.
XX
PD 02-JAN-2003.
XX
PF 19-NOV-2001; 2001US-00989734.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-352829/33.
DR P-PSDB; ABU72590.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
PT disease.
XX
PS Claim 1; Fig 327; 663pp; English.
XX
CC The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
CC are particularly useful for detecting or treating e.g. malignancies or
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
CC disease in mammals. The PRO polypeptides are useful in drug screening,
CC particularly as targets for therapeutic intervention in these diseases,
CC and in the diagnostic determination of the presence of these diseases.
CC The PRO polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide
XX
SQ Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.02e-141	Length:	2284
Score:	2211.00	Matches:	431
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-735-014-83 (1-431) x ACA64519 (1-2284)

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Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
              |||||||||||||||||||||||||||||||||
Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518
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RESULT 5
ABX96832
ID ABX96832 standard; cDNA; 2284 BP.
XX
AC ABX96832;
XX
DT 15-MAY-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO361.
XX
KW Human; ss; gene; PRO; secreted protein; transmembrane protein;

KW Cornelia de Lange syndrome; gene therapy; immune disorder;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defect; premature aging; cardiac injury; AIDS; cancer;
KW diabetic complication.
XX
OS Homo sapiens.
XX
PN US2002173463-A1.
XX
PD 21-NOV-2002.
XX
PF 31-AUG-2001; 2001US-00944944.
XX
PR 03-DEC-1997; 97US-0067411P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 16-DEC-1997; 97US-0069694P.
PR 16-DEC-1997; 97US-0069696P.
PR 16-DEC-1997; 97US-0069702P.
PR 17-DEC-1997; 97US-0069870P.
PR 17-DEC-1997; 97US-0069873P.
PR 18-DEC-1997; 97US-0068017P.
PR 05-JAN-1998; 98US-0070440P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-FEB-1998; 98US-0075945P.
PR 16-SEP-1998; 98WO-US019330.
PR 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 22-DEC-1998; 98US-0113296P.
PR 02-JUN-1999; 99WO-US012252.
PR 28-JUL-1999; 99US-0146222P.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 25-MAY-2001; 2001US-00866028.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
XX
DR WPI; 2003-311003/30.
DR P-PSDB; ABU64930.
XX
PT New transmembrane polypeptides and polynucleotides useful for chromosome
PT identification, tissue typing, gene therapy, in chromosome and gene
PT mapping, or as molecular weight markers.
XX
PS Claim 2; Fig 31; 172pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a secreted/
CC transmembrane polypeptide (designated as PRO proteins). 15 PRO
CC polypeptides and their encoding polynucleotides are disclosed. Also
CC included are a vector comprising the PRO nucleic acid, a host cell
CC comprising the vector, a process for producing a PRO polypeptide (by
CC culturing the host cell under conditions for the expression of the PRO
CC polypeptide, and recovering the PRO polypeptide from the cell culture, an
CC isolated polypeptide having at least 80% amino acid sequence identity to
CC the PRO polypeptides, a chimaeric molecule comprising PRO fused to a
CC heterologous amino acid sequence and an antibody which specifically binds
CC to PRO. The PRO nucleotide sequences are useful as hybridisation probes,
CC in chromosome and gene mapping, in generating sense and antisense RNA or
CC DNA, in generating transgenic or knock-out animals which can be used in
CC the development and screening of therapeutically useful reagents, and in
CC gene therapy. The polypeptides may be used as molecular weight markers
CC for protein electrophoresis purposes. The PRO polypeptides and nucleic
CC acids may also be used for chromosome identification, and tissue typing.
CC PRO241 (identified as Chordin) is a candidate gene for Cornelia de Lange
CC syndrome. Other PRO proteins are variously implicated in immune
CC disorders, inflammatory disease, organ failure, atherosclerosis, cardiac
CC injury, infertility, birth defects, premature aging, cardiac injury,
CC AIDS, cancer and diabetic complications. The present sequence encodes a
CC PRO protein
XX
SQ Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.02e-141	Length:	2284
Score:	2211.00	Matches:	431
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-735-014-83 (1-431) x ABX96832 (1-2284)

```
Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 ACCCTCATTTCTACAGTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
              |||||||||||||||||||||||||||||||
Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518
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```
RESULT 6
ABX78486
ID   ABX78486 standard; DNA; 2284 BP.
XX
AC   ABX78486;
XX
DT   14-APR-2003  (first entry)
XX
DE   DNA encoding Novel human secreted protein PRO361.
XX
KW   Human; antiinflammatory; antiarteriosclerotic; cardiant; gynecological;
KW   anti-HIV; cytostatic; antidiabetic; BMP-agonist; BMP-Antagonist;
KW   cytokine-agonist; cytokine-antagonist; gene-Therapy;
KW   inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW   infertility; birth defect; premature aging; AIDS; cancer;
KW   diabetic complication; gene; ds.
XX
OS   Homo sapiens.
XX
PN   US2002150976-A1.
XX
PD   17-OCT-2002.
XX
PF   30-AUG-2001; 2001US-00943851.
XX
PR   03-DEC-1997;   97US-0067411P.
PR   11-DEC-1997;   97US-0069278P.
PR   11-DEC-1997;   97US-0069334P.
PR   11-DEC-1997;   97US-0069335P.
PR   12-DEC-1997;   97US-0069425P.
PR   16-DEC-1997;   97US-0069694P.
PR   16-DEC-1997;   97US-0069696P.
PR   16-DEC-1997;   97US-0069702P.
PR   17-DEC-1997;   97US-0069870P.
PR   17-DEC-1997;   97US-0069873P.
PR   18-DEC-1997;   97US-0068017P.
PR   05-JAN-1998;   98US-0070440P.
PR   09-FEB-1998;   98US-0074086P.
PR   09-FEB-1998;   98US-0074092P.
PR   25-FEB-1998;   98US-0075945P.
PR   16-SEP-1998;   98WO-US019330.
PR   01-DEC-1998;   98WO-US025108.
PR   16-DEC-1998;   98US-00216021.
PR   16-DEC-1998;   98US-0112850P.
PR   22-DEC-1998;   98US-00218517.
PR   22-DEC-1998;   98US-0113296P.
PR   03-MAR-1999;   99US-00254311.
PR   02-JUN-1999;   99WO-US012252.
PR   28-JUL-1999;   99US-0146222P.
PR   15-SEP-1999;   99WO-US021090.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   16-DEC-1999;   99WO-US030095.
PR   11-FEB-2000; 2000WO-US003565.
PR   22-FEB-2000; 2000WO-US004414.
PR   02-MAR-2000; 2000WO-US005841.
PR   30-MAR-2000; 2000WO-US008439.
PR   22-MAY-2000; 2000WO-US014042.
PR   28-JUL-2000; 2000WO-US020710.
PR   01-DEC-2000; 2000WO-US032678.
PR   28-FEB-2001; 2001WO-US006520.
PR   25-MAY-2001; 2001US-00866028.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Botstein D,  Eaton DL,  Ferrara N,  Filvaroff E;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL;
PI   Hillan KJ,  Kljavin IJ,  Napier MA,  Roy MA,  Tumas D,  Wood WI;
XX
DR   WPI; 2003-198285/19.
DR   P-PSDB; ABU58364.
XX
PT   New isolated PRO polypeptide and encoding nucleic acids, useful for the
PT   diagnosis and treatment of disorders such as inflammatory disease,
PT   atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic
PT   complications.
XX
PS   Claim 2; Fig 31; 171pp; English.
XX
CC   The invention describes a novel isolated PRO polypeptide. The methods and
CC   compositions of the present invention are useful for the diagnosis and
CC   treatment of disorders such as inflammatory disease, organ failure,
CC   atherosclerosis, cardiac injury, infertility, birth defects, premature
CC   aging, AIDS, cancer, diabetic complications and mutations in general.
CC   This sequence encodes a novel human secreted PRO protein
XX
SQ   Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:              1.02e-141       Length:         2284
Score:                  2211.00         Matches:        431
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     8               Gaps:           0

US-10-735-014-83 (1-431) x ABX78486 (1-2284)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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```
Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60

Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80

Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100

Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120

Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140

Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160

Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180

Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200

Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220

Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240

Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260

Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280

Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300

Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320

Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340

Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360

Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380

Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400

Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420

Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431

Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518
```

RESULT 7
ABX77120
ID ABX77120 standard; cDNA; 2284 BP.
XX
AC ABX77120;
XX
DT 04-APR-2003 (first entry)
XX
DE cDNA encoding human PRO361 protein.
XX
KW Gene; ss; human; antiinflammatory; antiarteriosclerotic; cardiant;
KW anti-infertility; anti-HIV; cytostatic; antidiabetic; transmembrane;
KW antiinflammatory; anti-HIV; antiarteriosclerotic; cardiant; infertility;
KW anti-infertility; cytostatic; antidiabetic; gene therapy; birth defect;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW premature aging; AIDS; cancer; diabetic complication.
XX
OS Homo sapiens.
XX
PN US2002142958-A1.
XX
PD 03-OCT-2002.
XX
PF 30-AUG-2001; 2001US-00943762.
XX
PR 16-SEP-1998; 98WO-US019330.
PR 01-DEC-1998; 98WO-US025108.
PR 22-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 25-MAY-2001; 2001US-00866028.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
XX
DR WPI; 2003-174140/17.
DR P-PSDB; ABU57251.
XX
PT New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
PS Claim 2; Fig 31; 173pp; English.
XX
CC This invention relates to a nucleotide sequence encoding an isolated
CC secreted and/or transmembrane protein. The nucleotide sequences of the
CC invention may have antiinflammatory, antiarteriosclerotic, cardiant, anti
CC -infertility, anti-HIV, cytostatic and antidiabetic activities and may be

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CC   used in gene therapy. The nucleic acids and polypeptides are useful for
CC   treating inflammatory diseases, organ failure, atherosclerosis, cardiac
CC   injury, infertility, birth defects, premature aging, AIDS, cancer, or
CC   diabetic complications. The nucleic acids are useful as hybridisation
CC   probes, in chromosome and gene mapping, and in generating antisense RNA
CC   or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
CC   biosensors or bioreactors. Both are useful in tissue typing. The present
CC   sequence represents a nucleic acid sequence of the invention
XX
SQ   Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.02e-141      Length:          2284
Score:                    2211.00        Matches:         431
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       8              Gaps:            0

US-10-735-014-83 (1-431) x ABX77120 (1-2284)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 8
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ID   ABX80978 standard; cDNA; 2284 BP.
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AC   ABX80978;
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DT   22-APR-2003  (first entry)
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DE   Human secreted/transmembrane protein cDNA, #182.
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KW   Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;
KW   diagnostic; biosensor; bioreactor; tumour; therapeutic; gene therapy;
KW   tumour-associated antigenic target; TAT; ADEPT;
KW   antibody-dependent enzyme mediated prodrug therapy; cytostatic.
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OS   Homo sapiens.
XX
PN   US2003027162-A1.
XX
PD   06-FEB-2003.
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PF   15-NOV-2001; 2001US-00997428.
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PR   16-JUN-1997;   97US-0049787P.
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Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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AC   ACD44487;
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DT   10-SEP-2003  (first entry)
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DE   cDNA encoding human PRO361 polypeptide.
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KW   Human; PRO polypeptide; secreted protein; transmembrane protein;
KW   genetic disorder; antibacterial; immunosuppressive; transgenic;
KW   gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2002127576-A1.
XX
PD   12-SEP-2002.
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PF   14-NOV-2001; 2001US-00991073.
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PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-340824/32.
DR P-PSDB; ABO26036.
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT and are therapeutically useful for enhancing immune responses.
XX
PS Claim 2; Fig 327; 661pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The polynucleotide sequences
CC encoding PRO polypeptides are useful as hybridisation probes, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC in the preparation of PRO polypeptides, for generating transgenic animals
CC or knockout animals, to construct hybridisation probes for mapping the
CC gene which encodes the PRO polypeptide, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, for chromosome
CC identification, as chromosome markers, and for generating probes for PCR,
CC Northern analysis, Southern analysis and Western analysis. The present
CC sequence encodes a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.02e-141	Length:	2284
Score:	2211.00	Matches:	431
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-735-014-83 (1-431) x ACD44487 (1-2284)

```
Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 ACCCTCATTTCTACAGTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
              |||||||||||||||||||||||||||||||||
Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518
```

RESULT 10
ABX75951
ID ABX75951 standard; cDNA; 2284 BP.
XX
AC ABX75951;
XX
DT 31-MAR-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein, PRO361.
XX
KW Human; ss; gene; PRO; antiinflammatory; antiarteriosclerotic; cardiant;
KW gynecological; anti-HIV; cytostatic; antidiabetic; inflammatory disease;
KW organ failure; atherosclerosis; cardiac injury; infertility;
KW birth defect; premature aging; AIDS; acquired immunodeficiency syndrome;
KW cancer; diabetic complication.
XX
OS Homo sapiens.
XX
PN US2002132981-A1.
XX
PD 19-SEP-2002.
XX
PF 30-AUG-2001; 2001US-00944396.
XX
PR 03-DEC-1997; 97US-0067411P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 16-DEC-1997; 97US-0069694P.
PR 16-DEC-1997; 97US-0069696P.
PR 16-DEC-1997; 97US-0069702P.
PR 17-DEC-1997; 97US-0069870P.
PR 17-DEC-1997; 97US-0069873P.
PR 18-DEC-1997; 97US-0068017P.
PR 05-JAN-1998; 98US-0070440P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-FEB-1998; 98US-0075945P.
PR 16-SEP-1998; 98WO-US019330.
PR 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 22-DEC-1998; 98US-0113296P.
PR 02-JUN-1999; 99WO-US012252.
PR 28-JUL-1999; 99US-0146222P.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 25-MAY-2001; 2001US-00866028.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
XX
DR WPI; 2003-147446/14.
DR P-PSDB; ABU56315.

```
XX
PT   New isolated PRO polypeptide and encoding nucleic acids, useful for the
PT   diagnosis and treatment of disorders such as inflammatory disease,
PT   atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic
PT   complications.
XX
PS   Claim 2; Fig 31; 171pp; English.
XX
CC   The invention relates to an isolated PRO polypeptide having at least 80%
CC   amino acid sequence identity to and scoring at least 80% positives when
CC   compared to any of 15 fully defined sequences of 235-954 amino acids,
CC   given in the specification. Also included are: (1) an isolated PRO
CC   nucleic acid having at least 80% nucleic acid sequence identity to a
CC   nucleotide sequence that encodes PRO or its extracellular domain, and
CC   comprising any of 15 fully defined nucleotide sequences of 957-3441 bp,
CC   given in the specification and deposited under ATCC accession number
CC   209526, 209508, 209524, 209528, 209530, 209523, 209492, 209532, 209531,
CC   209529, 209527, 209570, 209618, 209621 and 209619; (2) a vector
CC   comprising the PRO nucleic acid; (3) a host cell comprising the vector;
CC   (4) producing PRO polypeptides, comprising culturing the cell for
CC   expression of the PRO polypeptide and recovering the PRO polypeptide from
CC   the cell culture; (5) a chimaeric molecule comprising PRO fused to a
CC   heterologous amino acid sequence; and (6) an anti-PRP antibody. The
CC   methods and compositions are useful for the diagnosis and treatment of
CC   disorders such as inflammatory disease, organ failure, atherosclerosis,
CC   cardiac injury, infertility, birth defects, premature aging, AIDS
CC   (acquired immunodeficiency syndrome), cancer, diabetic complications and
CC   mutations in general. The present sequence is a cDNA encoding a PRO
CC   polypeptide
XX
SQ   Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.02e-141      Length:          2284
Score:                    2211.00        Matches:         431
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       8              Gaps:            0

US-10-735-014-83 (1-431) x ABX75951 (1-2284)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
              |||||||||||||||||||||||||||||||||
Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 11
ABX89662
ID   ABX89662 standard; cDNA; 2284 BP.
XX
AC   ABX89662;
XX
DT   28-APR-2003  (first entry)
XX
DE   cDNA encoding novel secreted and transmembrane protein PRO361.
XX
KW   Secreted and transmembrane polypeptide; PRO; tissue typing; gene therapy;
KW   transgenic; knockout animal; inflammatory disease; organ failure;
KW   atherosclerosis; cardiac injury; infertility; birth defect;
KW   premature aging; acquired immunodeficiency syndrome; AIDS; cancer;
KW   diabetic complication; immune system disorder; proteoglycan release;
KW   sports-related joint problem; human; articular cartilage defect;
```

KW osteoarthritis; rheumatoid arthritis;
KW vascular endothelial cell growth factor stimulated proliferation;
KW endothelial cell growth; VEGF stimulated proliferation; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002168715-A1.
XX
PD 14-NOV-2002.
XX
PF 31-AUG-2001; 2001US-00944896.
XX
PR 03-DEC-1997; 97US-0067411P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 16-DEC-1997; 97US-0069694P.
PR 16-DEC-1997; 97US-0069696P.
PR 16-DEC-1997; 97US-0069702P.
PR 17-DEC-1997; 97US-0069870P.
PR 17-DEC-1997; 97US-0069873P.
PR 18-DEC-1997; 97US-0068017P.
PR 05-JAN-1998; 98US-0070440P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-FEB-1998; 98US-0075945P.
PR 16-SEP-1998; 98WO-US019330.
PR 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-00216021.
PR 16-DEC-1998; 98US-0112850P.
PR 22-DEC-1998; 98US-00218517.
PR 22-DEC-1998; 98US-0113296P.
PR 03-MAR-1999; 99US-00254311.
PR 22-JUN-1999; 99WO-US012252.
PR 28-JUL-1999; 99US-0146222P.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 25-MAY-2001; 2001US-00866028.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
XX
DR WPI; 2003-275322/27.
DR P-PSDB; ABU60355.
XX
PT Novel isolated PRO polypeptides e.g. PRO243, PRO299, PRO323, PRO327,
PT PRO344, and polynucleotides useful in the treatment of human disorders
PT related to immune system, and in gene therapy.
XX
PS Claim 2; Fig 31; 173pp; English.
XX
CC The invention describes an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide (I) having at least 80 %
CC identity to, a 379, 954, 737, 433, 422, 300, 243, 455, 694, 440, 598,
CC 250, 281, 431 or 235 amino acid sequence (S1), given in the
CC specification, S1 lacking its associated signal peptide or extracellular
CC domain of S1 with or without its associated signal peptide. (I) and the
CC polynucleotide (II) encoding it are useful in tissue typing and gene
CC therapy. (II) is also useful for generating transgenic animals or
CC knockout animals for the development and screening of therapeutically
CC useful reagents. PRO233 polypeptide is useful for treating inflammatory
CC disease, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer and diabetic complications. The other PRO polypeptides
CC including PRO243, PRO299, PRO323, PRO327, PRO344, PRO347, PRO354, PRO355,
CC PRO715, PRO353, PRO361 and PRO365 are useful for treating human disorders
CC involving the immune system. PRO241 is useful for stimulating release of
CC proteoglycans from cartilage, and thus for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis and rheumatoid
CC arthritis. (I) is also useful for inhibiting vascular endothelial cell
CC growth factor (VEGF) stimulated proliferation of endothelial cell growth.
CC This sequence encodes a novel human secreted and transmembrane protein
XX
SQ Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.02e-141	Length:	2284
Score:	2211.00	Matches:	431
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-735-014-83 (1-431) x ABX89662 (1-2284)

```
Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

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Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 12
ABX79658
ID   ABX79658 standard; cDNA; 2284 BP.
XX
AC   ABX79658;
XX
DT   17-APR-2003  (first entry)
XX
DE   Human sectreted/transmembrane protein cDNA, #182.
XX
KW   Human; gene; ss; PRO; secreted; transmembrane; signal peptide;
KW   pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;
KW   colon cancer; lung cancer; breast cancer; cancer; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2002142961-A1.
XX
PD   03-OCT-2002.
XX
PF   19-NOV-2001; 2001US-00989721.
XX
PR   16-JUN-1997;   97US-0049787P.
PR   17-OCT-1997;   97US-0062250P.
PR   05-NOV-1997;   97WO-US020069.
PR   12-NOV-1997;   97US-0065186P.
PR   13-NOV-1997;   97US-0065311P.
PR   24-NOV-1997;   97US-0066770P.
PR   25-FEB-1998;   98US-0075945P.
PR   20-MAR-1998;   98US-0078910P.
PR   28-APR-1998;   98US-0083322P.
PR   07-MAY-1998;   98US-0084600P.
PR   28-MAY-1998;   98US-0087106P.
PR   02-JUN-1998;   98US-0087607P.
PR   02-JUN-1998;   98US-0087609P.
PR   02-JUN-1998;   98US-0087759P.
PR   03-JUN-1998;   98US-0087827P.
PR   04-JUN-1998;   98US-0088021P.
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PR   05-JUN-1998;   98US-0088202P.
PR   05-JUN-1998;   98US-0088212P.
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PR   10-JUN-1998;   98US-0088742P.
PR   10-JUN-1998;   98US-0088810P.
PR   10-JUN-1998;   98US-0088824P.
PR   10-JUN-1998;   98US-0088826P.
PR   11-JUN-1998;   98US-0088858P.
PR   11-JUN-1998;   98US-0088861P.
PR   11-JUN-1998;   98US-0088876P.
PR   12-JUN-1998;   98US-0089105P.
PR   16-JUN-1998;   98US-0089440P.
PR   16-JUN-1998;   98US-0089512P.
PR   16-JUN-1998;   98US-0089514P.
PR   17-JUN-1998;   98US-0089532P.
PR   17-JUN-1998;   98US-0089538P.
PR   17-JUN-1998;   98US-0089598P.
PR   17-JUN-1998;   98US-0089599P.
PR   17-JUN-1998;   98US-0089600P.
PR   17-JUN-1998;   98US-0089653P.
PR   18-JUN-1998;   98US-0089801P.
PR   18-JUN-1998;   98US-0089907P.
PR   18-JUN-1998;   98US-0089908P.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   02-JUN-1999;   99WO-US012252.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   30-MAR-2000; 2000WO-US008439.
PR   15-MAY-2000; 2000WO-US013358.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
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PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-155950/15.
DR P-PSDB; ABU59045.
XX
PT New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,
PT PRO361 or PRO846) useful as targets for therapeutic intervention in
PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers.
XX
PS Claim 2; Fig 327; 647pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful as pharmaceuticals, diagnostics,
CC biosensors or bioreactors, for detecting or treating e.g. tumours in
CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or
CC rabbits as targets for therapeutic intervention in certain cancers (e.g.
CC colon, lung or breast cancers) and diagnostic determination of the
CC presence of these cancers. The PRO polypeptides are also useful as
CC molecular weight markers or for chromosome identification. The PRO genes
CC are useful as hybridisation probes or for screening libraries of human
CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC therapy, particularly for replacing a defective gene. The sequences
CC presented in ABX79290-ABX79675 are the genes encoding, the primers
CC amplifying and the probes detecting the PRO polynucleotides of the
CC invention. Note: The sequence data for this patent is also available in
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.02e-141	Length:	2284
Score:	2211.00	Matches:	431
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-735-014-83 (1-431) x ABX79658 (1-2284)

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Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485
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RESULT 13
ACA93679
ID   ACA93679 standard; cDNA; 2284 BP.
XX
AC   ACA93679;
XX
DT   16-JUL-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO361 cDNA.
XX
KW   Human; secreted and transmembrane protein; PRO; PRO183; PRO184; PRO185;
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KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosum; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;
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US-10-735-014-83 (1-431) x ABX81361 (1-2284)

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KW neuroprotective; antiparkinsonian; cytostatic; gene therapy;
KW chromosome mapping; gene mapping; transgenic animal; knock-out animal;
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
KW gene; ss.
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XX
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PD 23-JAN-2003.
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US-10-735-014-83 (1-431) x ACA93177 (1-2284)

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Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Search completed: April 26, 2005, 22:36:16
Job time : 632 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 26, 2005, 22:02:22 ; Search time 223 Seconds
(without alignments)
3162.490 Million cell updates/sec

Title: US-10-735-014-83
Perfect score: 2211
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2211	100.0	2284	4	US-09-866-028-82	Sequence 82, Appl
2	2211	100.0	2284	4	US-09-944-457-82	Sequence 82, Appl
3	242	10.9	295	4	US-09-513-999C-9897	Sequence 9897, Ap
4	194.5	8.8	1642	4	US-09-489-847-70	Sequence 70, Appl
5	193	8.7	1826	4	US-09-774-528-230	Sequence 230, App
6	160.5	7.3	1638	4	US-09-799-451-412	Sequence 412, App
7	157	7.1	16562	4	US-09-949-016-13892	Sequence 13892, A
8	152	6.9	1297	4	US-09-976-594-950	Sequence 950, App
9	148	6.7	2032	3	US-09-241-581B-5	Sequence 5, Appli
10	148	6.7	2032	3	US-08-265-428-5	Sequence 5, Appli
11	148	6.7	2032	5	PCT-US95-07721-5	Sequence 5, Appli
c 12	146	6.6	767677	4	US-09-949-016-12147	Sequence 12147, A
c 13	146	6.6	767677	4	US-09-949-016-17361	Sequence 17361, A
c 14	145.5	6.6	2114	3	US-09-370-838-158	Sequence 158, App
c 15	145.5	6.6	2114	4	US-09-854-133-158	Sequence 158, App
c 16	145	6.6	9636	1	US-08-323-170B-1	Sequence 1, Appli
c 17	145	6.6	9636	3	US-08-954-441-1	Sequence 1, Appli
18	144.5	6.5	3423	4	US-09-614-221A-91	Sequence 91, Appl
19	141.5	6.4	3486	4	US-09-614-221A-292	Sequence 292, App
c 20	140	6.3	12685	4	US-09-479-467A-3	Sequence 3, Appli
21	138.5	6.3	3159	3	US-09-437-054A-7	Sequence 7, Appli
22	135	6.1	2150	2	US-08-861-464-13	Sequence 13, Appl
23	135	6.1	2150	2	US-08-396-001-13	Sequence 13, Appl
24	135	6.1	2150	3	US-09-323-433A-13	Sequence 13, Appl
25	135	6.1	2150	4	US-09-826-752-13	Sequence 13, Appl
26	134	6.1	5163	3	US-08-700-651-1	Sequence 1, Appli
27	134	6.1	5163	3	US-08-928-361B-4	Sequence 4, Appli
28	134	6.1	5163	4	US-09-588-995A-4	Sequence 4, Appli
29	134	6.1	5318	3	US-08-700-651-2	Sequence 2, Appli
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32	133.5	6.0	867	4	US-09-216-393B-340	Sequence 340, App
33	133.5	6.0	867	4	US-09-216-393B-342	Sequence 342, App
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37	133	6.0	1671	4	US-09-614-221A-554	Sequence 554, App
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40	132	6.0	2821	3	US-09-103-429A-2	Sequence 2, Appli
41	132	6.0	2821	4	US-09-294-663-2	Sequence 2, Appli
42	132	6.0	5511	3	US-08-928-361B-2	Sequence 2, Appli
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44	132	6.0	7334	3	US-08-928-361B-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
US-09-866-028-82
; Sequence 82, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 82
; LENGTH: 2284
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-866-028-82

Alignment Scores:
Pred. No.: 1.97e-217 Length: 2284

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Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     4             Gaps:          0

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Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

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Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

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Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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; Patent No. 6734288
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,457
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,694
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,702
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/069,873
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
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;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. 6734288ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. 6734288ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: Decemberl, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 82
;   LENGTH: 2284
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-944-457-82

Alignment Scores:
Pred. No.:                1.97e-217      Length:          2284
Score:                    2211.00        Matches:         431
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       4              Gaps:            0

US-10-735-014-83 (1-431) x US-09-944-457-82 (1-2284)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
                    |||||||||||||||||||||||||||||||
Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 3
US-09-513-999C-9897
; Sequence 9897, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 9897
;   LENGTH: 295
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 58
;   OTHER INFORMATION: r=a or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 59
;   OTHER INFORMATION: w=a or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 69
;   OTHER INFORMATION: r=a or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 82
;   OTHER INFORMATION: r=a or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 83
;   OTHER INFORMATION: w=a or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 126
;   OTHER INFORMATION: k=g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 129
;   OTHER INFORMATION: m=a or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 133
;   OTHER INFORMATION: m=a or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 136
;   OTHER INFORMATION: r=a or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 158
;   OTHER INFORMATION: b=c or g or t
US-09-513-999C-9897

Alignment Scores:
Pred. No.:                6.49e-16        Length:          295
Score:                    242.00          Matches:         54
Percent Similarity:       91.53%          Conservative:    0
Best Local Similarity:    91.53%          Mismatches:      3
Query Match:              10.95%          Indels:          2
DB:                       4               Gaps:            0

US-10-735-014-83 (1-431) x US-09-513-999C-9897 (1-295)

Qy        375 AsnGlnTyrGlyLeuProPheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyVal 394
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATCAGTACGGCCTTCCATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTRWC 60

Qy        395 LeuPheLeuValIleGlyLeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArg 414
                    ||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db         61 CTGTTCCTRGTGATAGGCCTCRWCCTCCTGGGTAGAATCCTCTCGGAATCACTCCGCAGG 120

Qy        415 LysArg-TyrSerArg-LeuAspTyrLeuIleAsnGlyIleTyrValAspIle 431
                    ||||||    |||||| ||||||||||||||||||||||||||||||||||||
Db        121 AAACGKTAMCTCMAGRACTGGATTACTTGATCAATGGBATCTATGTGGACATC 173

RESULT 4
US-09-489-847-70
; Sequence 70, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al
;  TITLE OF INVENTION: 98 Human Secreted Proteins
;  FILE REFERENCE: PZ031P1
;  CURRENT APPLICATION NUMBER: US/09/489,847
;  CURRENT FILING DATE: 2000-01-24
;  EARLIER APPLICATION NUMBER: PCT/US99/17130
;  EARLIER FILING DATE: 1999-07-29
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  EARLIER APPLICATION NUMBER: 60/095,486
;  EARLIER FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: 60/096,319
;  EARLIER FILING DATE: 1998-08-12
;  EARLIER APPLICATION NUMBER: 60/095,454
;  EARLIER FILING DATE: 1998-08-06
;  EARLIER APPLICATION NUMBER: 60/095,455
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 376
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
;   LENGTH: 1642
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-489-847-70

Alignment Scores:
Pred. No.:                1.07e-09        Length:          1642
Score:                    194.50          Matches:         105
Percent Similarity:       37.06%          Conservative:    64
Best Local Similarity:    23.03%          Mismatches:      166
Query Match:              8.80%           Indels:          121
DB:                       4               Gaps:            20

US-10-735-014-83 (1-431) x US-09-489-847-70 (1-1642)

Qy         20 ThrLeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIle 39
                  ::::::   |||:::|||:::   :::   |||   |||       |||      :::
Db        289 AGCATCYCCTTAGCAGCAGCCTCTGATCCCTTGGCCAAGCAG---GAGGGAACCATTAGC 345

Qy         40 AspIleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThr 59
                    :::::::|||   |||:::   |||       |||:::   |||
Db        346 AGCCTGAGGAGCTGGCTGGCT---GGGAGCCTCGGGGACCGCCCAGCCTTGCTCCCAGCT 402

Qy         60 GlnGluAspCysIleAsnSerCysCysSerThrLysAsn---------IleSerGlyAsp 76
                       :::::::|||   |||:::      :::         :::
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Db        403 CACCCACAAGATGTGGACAGCTCTTGTGCTCATTTGGATTTTYTCCTTGTCCTTATCTGA 462

Qy         77 LysAlaCysAsnLeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyr  96

Db        463 AAGCCATGCGGCATCCAA-----------CGATCCACG--------------------- 489

Qy         97 LeuPhePheCysProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeu------ 114

Db        490 --------------------CAACTTTGTCCCTAACAAAATGTGGAAGGGATTAGTCAA 528

Qy        115 ------------------------------------------------------------Met 115

Db        529 GAGGAATGCATCTGTGGAAACAGTTGATAATAAAACGTCTGAGGATGTAACCATGGCAGC 588

Qy        116 SerTyrArgIleIleThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeu 135

Db        589 AGCTTCTCCTGTCACATTGACCAAAGGGATTCGGCAGCCCAMCTCAACTCTATGGAAGTC 648

Qy        136 ProGlnGluAspSerLeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHis 155

Db        649 ACAACAGAGGACACA------------------------------------------- 663

Qy        156 HisHisThrAspTyrSerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLys 175

Db        664 AGCAGGACAGATGTGAGTGAACCA-------------------------GCAACTTCA 696

Qy        176 PheGlySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeu 195

Db        697 GGAGGTGCAGCTGATGGTGTGACCTCCATTGCTCCCACGGCTGTGGCCTCCAGTACGACT 756

Qy        196 LeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIle 215

Db        757 GCGGCC--------------------TCCATTACGACTGCGGCCTCCAGTATGACTGTG 795

Qy        216 AlaHisLeuLeuProGluAsnValSerAlaLeuProAlaThrValAlaValAlaSerPro 235

Db        796 GCCTCCAGTGCTCCC---ACGACTGCAGCCTCCAGTACAACTGTGGCCTCCATTGCTCCC 852

Qy        236 HisThr---------------ThrSerAlaThrProLysProAlaThrLeu---LeuPro 249

Db        853 ACGACTACAGCCTCCAGTATGACTGCGGCCTCCAGCACTCCCATGACACTTGCACTCCCC 912

Qy        250 ThrAsnAlaSerVal------------ThrProSer------GlyThrSerGlnProGln 263

Db        913 GCGCCCACGTCCACTTYCACAGGGCGGACCCCGTCCACTACCGCCACTGGGCATCCATCT 972

Qy        264 LeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThrThrLeuIle 283

Db        973 CTCAGCACAGCCCTCGCACAAGTGCCAAAGAGCAGCGCGTTGCCAAGAACAGCAACCCTG 1032

Qy        284 SerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThrAlaValLeu 303

Db       1033 GCCACATTGGCCACACGTGCT------------CAGACTGTAGCGACCACAGCAAACACA 1080

Qy        304 ThrThrThrPheGlnAla---ProThrAspSerLysGlySerLeuGluThrIleProPhe 322

Db       1081 AGCAGCCCCATGAGCACTCGTCCAAGTCCTTCCAAGCACATGCCCAGTGACACCGCGGCA 1140

Qy        323 ThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla------ 340

Db       1141 AGCCCTGTACCCCCTATGCKT-----------------CCCCAAGCACAAGGT 1176

Qy        341 ---LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGly 359

Db       1177 CCCATTAGCCAGGTGTCAGTGGACCAGCCTGTGGTTAACACAACA-------------- 1221

Qy        360 ArgGluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeu 379

Db       1222 --------------------WATAAATCCACAMCCATGCCCTCAAACACAACCMCWGAG 1260

Qy        380 ProPhe--------------GluLysTrpLeuLeuIleGlySerLeuLeuPheGlyVal 394

Db       1261 CCCCTCACCCAGGCCGTGGTAGACAAAACTCTCCTTCTGGTGGTGCTGTTACTCGGGGTG 1320

Qy        395 LeuPheLeuValIleGlyLeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArg 414

Db       1321 ACCCTTTTCATCACAGTCTTGGTTTTGTTTGCCCTGCAGGCCTATGAGAGCTACAAGAAG 1380

Qy        415 LysArgTyrSerArgLeuAspTyrLeuIleAsnGlyIleTyrValAsp 430

Db       1381 AAGGACTACACCCAGGTGGACTACTTAATCAACGGGATGTATGCGGAC 1428
```

RESULT 5
US-09-774-528-230
; Sequence 230, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 230
; LENGTH: 1826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (415)..(1764)
US-09-774-528-230

Alignment Scores:

Pred. No.:	1.85e-09	Length:	1826
Score:	193.00	Matches:	126
Percent Similarity:	34.50%	Conservative:	61
Best Local Similarity:	23.25%	Mismatches:	170
Query Match:	8.73%	Indels:	187
DB:	4	Gaps:	23

US-10-735-014-83 (1-431) x US-09-774-528-230 (1-1826)

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Qy         20 ThrLeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIle 39

Db        291 AGCATCCCCTTAGCAGCAGCCTCTGATCCCTTGGCCAAGCAG---GAGGGAACCATTAGC 347

Qy         40 AspIleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThr 59

Db        348 AGCCTGAGGAGCTGGCTGGCTGGGAGCCT-CGGGGACCGCCCAGCCTTGCTCCCAGCTCA 406

Qy         60 GlnGluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCys 79

Db        407 CCCACAAGATGTGGACAGCTCTTGTGCTCA------------TTTGGATTTTCTCCTTGT 454

Qy         80 AsnLeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePhe 99

Db        455 CCTTATCTG--------------AAAGCCATGCGGCATCCAACGATCCACGCAAC-TTT 498

Qy        100 CysProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMet------------ 115

Db        499 GTCCCTAAC-----------------AAAATGTGGAAGGGATTAGTCAAGAGGAATGCA 540
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Qy        116 SerTyrArgIleIleThrAspPheProSer---------------------------- 125
              |||         :::   :::      |||
Db        541 TCTGTGGAAACAGTTGATAATAAAACGTCTGAGGATGTAACCATGGCAGCAGCTTCTCCT 600

Qy        126 ------LeuThrArg--------------AsnLeuProSerGlnGluLeuProGlnGlu 138
                  ||||||:::                :::|||   |||   |||:::      |||
Db        601 GTCACATTGACCAAAGGGACTTCGGCAGCCCACCTCAACTCTATGGAAGTCACAACAGAG 660

Qy        139 AspSerLeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThr 158
              |||:::                                                  |||
Db        661 GACACA-----------------------------------------------AGCAGGACA 675

Qy        159 AspTyrSerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySer 178
              |||   |||:::|||                        :::             :::
Db        676 GATGTGAGTGAACCA-------------------------GCAACTTCAGGAGTTGCA 708

Qy        179 SerAspHisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyr 198
              :::|||   :::      :::                |||||:::        |||
Db        709 GCTGATGGTGTGACCTCCATTGCTCCCACGGCTGTGGCCTCCAGTACGACTGCGGCC--- 765

Qy        199 LysGluLysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeu 218
                          :::      :::|||         :::|||
Db        766 -----------------TCCATTACGACTGCGGCCTCCAGTATGACTGTGGCCTCCAGT 807

Qy        219 LeuProGluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThr--- 237
              |||         :::|||         ||||||||      :::|||   |||
Db        808 GCTCCC---ACGACTGCAGCCTCCAGTACAACTGTGGCCTCCATTGCTCCCACGACTGCA 864

Qy        238 ------------ThrSerAlaThrProLysProAlaThrLeu---------LeuProThr 250
                         |||:::|||:::      |||   ||||||           ||||||
Db        865 GCCTCCAGTATGACTGCGGCCTCCAGCACTCCCATGACACTTGCACTCCCCGCGCCCACG 924

Qy        251 AsnAlaSerVal------ThrProSer------GlyThrSerGlnProGlnLeuAlaThr 266
              :::   |||         |||||||||         |||      |||   |||:::|||
Db        925 TCCACTTCCACAGGGCGGACCCCGTCCACTACCGCCACTGGGCATCCATCTCTCAGCACA 984

Qy        267 ThrAlaProProValThrThrValThrSerGlnProProThrThrLeuIleSerThrVal 286
                        |||         ::::::   |||   |||      ::::::|||:::
Db        985 GCCCTCGCACAAGTGCCAAAGAGCAGCGCGTTGCCAAGAACAGCAACCCTGGCCACATTG 1044

Qy        287 PheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThrAla--------------- 301
              |||||||||           |||   :::|||||||||||||
Db       1045 GCCACACGTGCT------------CAGACTGTAGCGACCACAGCAAACACAAGCAGCCCC 1092

Qy        301 ------------------------------------------------------------ 301

Db       1093 ATGAGCACTCGTCCAAGTCCTTCCAAGCACATGCCCAGTGACACCGCGGCAAGCCCTGTA 1152

Qy        301 ------------------------------------------------------------ 301

Db       1153 CCCCCTATGCGTCCCCAAGCACAAGGTCCCATTAGCCAGGTGTCAGTGGACCAGCCTGTG 1212

Qy        302 ValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIlePro 321
              |||   ||||||          |||      |||      :::   |||      |||
Db       1213 GTTAACACAACAAATAAATCCACACCCATGCCCTCAAACACAACCCCAGAGCCCGCCCCC 1272

Qy        322 PheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAlaLeu 341
                    :::      :::|||                                |||||||||
Db       1273 ACCCCCACAGTG------GTGACCACCACCAAGGCACAAGCCAGGGAGCCAACTGCCAGC 1326

Qy        342 ----------------------------------------SerMetSer---AsnVal 346
                                                     :::||||||
Db       1327 CCAGTGCCAGTACCTCACACCAGGCCAATCCCTGAGATGGAGGCCATGTCCCCCACGACA 1386

Qy        347 GluSerSerThrMetAsnLysThrAlaSerTrpGluGly--------------------- 359
              ::::::|||   |||      |||         |||
Db       1387 CAGACAAGCCCCATGCCATATACCCAGAGGGACGCTGGGCCAGGCACATCCCAGGCACCG 1446

Qy        360 ------------ArgGluAlaSerProGlySerSerSerGlnGlySerValProGluAsn 375
                         ||||||:::||||||:::   |||   |||      |||   :::
Db       1447 GAGCAGGTAGAGACTGAAGCCACACCAGGTACTGATTCCACTGGGCCAACACCCAGGAGC 1506

Qy        376 GlnTyrGly------LeuPro---------------------------------------- 380
                    |||      :::|||
Db       1507 TCAGGGGGCACTAAGATGCCAGCCACGGACTCGTGCCAGCCCAGCACCCAAGGCCAGTAC 1566

Qy        381 ------------------------------------PheGluLysTrpLeuLeuIleGly 388
                                                 :::|||   ||||||:::
Db       1567 ATGGTGGTCACCACTGAGCCCCTCACCCAGGCCGTGGTAGACAAAACTCTCCTTCTGGTG 1626

Qy        389 SerLeuLeuPheGlyValLeuPheLeuValIleGlyLeuValLeuLeuGlyArgIleLeu 408
              ||||||   ||||||         :::      |||||||||
Db       1627 GTGCTGTTACTCGGGGTGACCCTTTTCATCACAGTCTTGGTTTTGTTTGCCCTGCAGGCC 1686

Qy        409 SerGluSerLeuArgArgLysArgTyrSerArgLeuAspTyrLeuIleAsnGlyIleTyr 428
              ||||||   :::::::|||   |||:::::::::|||||||||||||||||:::|||
Db       1687 TATGAGAGCTACAAGAAGAAGGACTACACCCAGGTGGACTACTTAATCAACGGGATGTAT 1746

Qy        429 ValAsp 430
              |||
Db       1747 GCGGAC 1752
```

RESULT 6
US-09-799-451-412
; Sequence 412, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 412
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (325)..(1353)
US-09-799-451-412

Alignment Scores:

Pred. No.:	3.44e-06	Length:	1638
Score:	160.50	Matches:	66
Percent Similarity:	39.85%	Conservative:	42
Best Local Similarity:	24.35%	Mismatches:	114
Query Match:	7.26%	Indels:	49
DB:	4	Gaps:	9

US-10-735-014-83 (1-431) x US-09-799-451-412 (1-1638)

```
Qy        147 SerGlnAlaValThrProLeuAlaHisHisHisThrAspTyrSerLysProThrAspIle 166
              ||||||   ||||||         |||           ::::::|||      |||:::
Db         43 TCCCAACCAGTCACCAGAGACTGTCATCTCCGGTGCACCTGGACCAAGTGGTTTGACGTA 102
```

```
Qy       167 SerTrp--------------------------ArgAspThrLeuSerGlnLysPheGly 177
Db       103 GACTTCCCATCCCCTGGACCCCACGGCGGGGACAAGGAAACCTACAACAACATCATCAGG 162

Qy       178 SerSerAspHisLeu------------GluLysLeuPheLysMetAsp------------ 189
Db       163 AGTGGGGAAAAAATCTGCCGCCGACCTGAGGAGATCACCAGGCTCCAGTGCCGAGCCGAG 222

Qy       190 ---------GluAlaSerAlaGlnLeuLeuAlaTyr---------------LysGluLys 201
Db       223 AGCCACCCGGAGGTGAGCATTGAACACCTGGGCCAGGTGGTGCAGTGCAGCCGTGAAGAG 282

Qy       202 Gly---------------HisSerGlnSerSerGlnPheSerSer------AspGlnGlu 214
Db       283 GGCCTGGTGTGCCGGAACCAGGACCAGCAGGGACCCTTCAAGATGTGCCTCAACTACGAG 342

Qy       215 IleAlaHisLeuLeuProGluAsnValSerAlaLeuProAlaThrValAlaValAlaSer 234
Db       343 GTGCGTGTGCTCTGCTGCGAGACCCCTAAAGGTTGCCCCGTGACC---------TCCACA 393

Qy       235 ProHisThrThrSerAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSer--- 253
Db       394 CCTGTGACAGCTCCTAGCACCCCTAGTGGGAGAGCCACCAGCCCAACTCAGAGCACTTCC 453

Qy       254 ----------------------------ValThrProSerGlyThrSerGlnProGln 263
Db       454 TCTTGGCAGAAATCCAGGACAACCACTTTGGTGACAACCAGCACAACCTCCACTCCACAG 513

Qy       264 LeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThrThrLeuIle 283
Db       514 ACCAGCACAACCTCTGCTCCTACAACCAGCACAACCTCTGCTCCCACAACCAGCACAACT 573

Qy       284 SerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThrAlaValLeu 303
Db       574 TCTGCCCCTACAACCAGCACAACCTCCACTCCACAGACCAGCATATCCTCTGCCCCTACA 633

Qy       304 ThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThr---------Ile 320
Db       634 AGCAGCACAACCTCGGCTCCTACAAGCAGCACAATCTCTGCTCGTACAACCAGCATAATC 693

Qy       321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
Db       694 TCTGCCCCTACAACCAGCACAACCTCTTTCCCTACAACCAGCACAACCTCTGCTACTACA 753

Qy       341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
Db       754 ACCAGCACAACCTCTGCCCCTACAAGCAGCACAACCTCCACTCCACAGACCAGCAAAACC 813

Qy       361 GluAlaSerProGlySerSerSerGlnGlySer 371
Db       814 TCAGCTGCTACAAGCAGCACAACCTCCGGTTCT 846
```

RESULT 7
US-09-949-016-13892
; Sequence 13892, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13892
; LENGTH: 16562
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13892

Alignment Scores:

Pred. No.:	0.000474	Length:	16562
Score:	157.00	Matches:	106
Percent Similarity:	33.97%	Conservative:	55
Best Local Similarity:	22.36%	Mismatches:	176
Query Match:	7.10%	Indels:	137
DB:	4	Gaps:	21

US-10-735-014-83 (1-431) x US-09-949-016-13892 (1-16562)

```
Qy        22 ArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAspIle 41
Db      6133 AGGGCCTCCCATCTCCCCAGCTGCCTTAGCTCTAGCCTCTCCCATGATAGCTCCAACTCT 6192

Qy        42 Gln-----------------SerSerLeuSerLysGlyIleArgGlyAsnGluProVal 55
Db      6193 GAAAGGGACCCCTTCCTCTTCAGCTCCCTTAGCTCTGGTTGCCCTGGCTCCCCA------ 6246

Qy        56 TyrThrSerThrGlnGluAspCysIleAsn--------------------------Ser 66
Db      6247 ---CTCAGTTCAGAAGAGTTCTGCTTTTCCACCTAACCTTCTTACTTCACCTCCTTCAGT 6303

Qy        67 CysCysSerThrLysAsnIleSerGlyAspLysAla---------CysAsnLeuMetIle 83
Db      6304 GGCTGTAGCTGAGTCAGGGTCAGTGATAACTCTGTCAGCTCCCATTGCTCCCTCAGAACC 6363

Qy        84 PheAsp---------------------------------ThrArgLysThrAlaArgGln 92
Db      6364 AAAGACTAATCTTAATAAAGTTCCCTCTGAGGTAGTCCCTAATCCAAAAGGCACCCCCAG 6423

Qy        93 ProAsnCysTyrLeuPhePheCysProAsnGluGluAlaCysProLeuLysProAlaLys 112
Db      6424 CCCTCCATGTATAGTCAGTACTGT-----------TCCTTACCACTGTGTGACTCCCAT 6471

Qy       113 GlyLeuMetSerTyrArgIleIleThrAspPheProSerLeu------ThrArgAsnLeu 130
Db      6472 GGCCTC------TATTCAATCTGGAGTGGCCTCCCTTCCTCAGACAACACCCACAACTAC 6525

Qy       131 ProSerGlnGluLeuProGlnGluAspSerLeuLeuHisGlyGlnPheSerGlnAlaVal 150
Db      6526 CCTAGCCATCGCTTCCCCTCAAGTCAA-------------------------------- 6552

Qy       151 ThrProLeuAlaHisHisHis---------ThrAspTyrSer---LysProThr-AspIl 166
Db      6553 ---------AGATACCACCATTTCCTCAGTTCTGATTTCTCCACAAAACCCAGGAAGCCT 6603

Qy       166 eSerTrpArgAsp---------------------------------------------- 170
Db      6604 CAGCCTGAAGGGGCCTGTTAGTCCACCTGCTGCCTTATCTCTTTCAACTCAGTCTCTTCC 6663

Qy       171 -------ThrLeuSerGlnLys--------------------------------PheGl 177
Db      6664 TGTGGTGACCTCTTCTCAAAAGACTGCGGGTCCCAACACCCCCCCAGATTTTCCCATTTC 6723

Qy       177 ySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAl 197
Db      6724 TCTGGGCTCTCATCTTGCACCTTTACATCAGAGTTCTTTTGGTTCTGTCCAACTTTTAGG 6783

Qy       197 aTyr---------------------------LysGluLys-----------GlyHisSe 204
Db      6784 TCAAACAGGTCCTAGTGCTTTGTCAGACCCTACAGAGAAGACCATTTCTGTAGATCATTC 6843

Qy       204 rGlnSer---SerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuProGluAsnVa 223
Db      6844 TTCCACAGGGGCCTCTTATCCTTCTCAGAGATCTGTAATTCCTCCCCTTCCTTCCAGAAA 6903

Qy       223 lSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAlaThrProLy 243
Db      6904 TGAGGTAGTTCCTGCTACTGTGGCTGCCTTTCCAGTGGTGGCTCCATCTGTTGACAAAGG 6963
```

```
Qy        243 sProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSerGlnProGl 263
Db       6964 TCCCTCTACCATC------TCTAGCATAACCTGCAGCCCTTCTGGCTCCTTAAATGTAGC 7017

Qy        263 nLeuAlaThrThrAlaProProValThrThr------ValThrSerGlnProProThrTh 281
Db       7018 TACCTCTTCTTCATTATCTCCTACAACCTCTCTCATTCTCAAAAGCTCTCCTAATGCCAC 7077

Qy        281 rLeu--------------------------IleSerThrValPheThrArgAlaAlaAl 292
Db       7078 TTATCATTATCCTTTAGTGGCCCAAATGCCCGTTTCTTCTGTTGGAACCACCCCACTTGT 7137

Qy        292 aThrLeuGlnAlaMetAlaThrThrAlaValLeuThrThrThrPheGln----------- 308
Db       7138 GGTGACTAACCCCTGTACAATTGCTGCAGCACCTACTACTACCTTTGAGGTAGCTACTTG 7197

Qy        309 ----AlaProThrAspSerLysGlySerLeuGluThrIle-------------------- 320
Db       7198 TGTTTCTCCTCCAATGTCATCAGGTCCCATAAGTAACATAGAACCAACTTCCCCTGCTGC 7257

Qy        321 ----------------------------ProPheThrGluIleSerAsnLeuThrLe 330
Db       7258 CTTGGTTATGGCACCTGTGGCTCCCAAAGAGCCTTCTACTCAAGTAGCAACCACTCTGAG 7317

Qy        330 uAsnThrGlyAsnValTyrAsnProThrAlaLeuSerMetSerAsnValGluSerSerTh 350
Db       7318 GATACCAGTCTCTCCTCCTCTGCCAGACCCTGAAGACCTCAAAAATCTCCCCAGTTCAGT 7377

Qy        350 rMetAsnLysThrAlaSerTrpGluGlyArgGluAlaSerProGlySerSerSerGlnGl 370
Db       7378 ATTGGTTAAATTTCCAACACAAAAAGACCTCCAAACTGTACCTGCCTCTCTTGAAGGAGC 7437

Qy        370 ySerValProGluAsnGlnTyrGlyLeuProPheGluLys 383
Db       7438 CCCTTTCTCTCCAGCCCAAGCAGGACTCACCACCAAGAAA 7477
```

RESULT 8
US-09-976-594-950
; Sequence 950, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 950
; LENGTH: 1297
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 1328310.1
US-09-976-594-950

Alignment Scores:

Pred. No.:	1.71e-05	Length:	1297
Score:	152.00	Matches:	65
Percent Similarity:	38.21%	Conservative:	50
Best Local Similarity:	21.59%	Mismatches:	111
Query Match:	6.87%	Indels:	75
DB:	4	Gaps:	12

US-10-735-014-83 (1-431) x US-09-976-594-950 (1-1297)

```
Qy        124 ProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSerLeuLeuHis 143
Db        367 CCAACACTCACGAGCGAGCTGTCCACCTCTCAGGCCGAGAACCAG------------CAC 414

Qy        144 GlyGlnPheSerGlnAlaValThrProLeuAla---HisHisHisThrAspTyrSerLys 162
Db        415 GCCCAGGACAGAGACGACAATGAGCCCCTTGACTAACACCACCACCAGCCAGGGCACGAC 474

Qy        163 Pro------ThrAspIle-SerTrpArgAspThrLeuSerGlnLysPhe----------- 176
Db        475 CCGCTGTCAACCGAAGTGTGAGTGGACAGAGTGGTTTGACGTGGACTTCCCAACCTCAGG 534

Qy        177 ----------GlySerSerAspHisLeuGluLysLeu---------------------- 185
Db        535 GGTTGCAGGCGGGGACATGGAAACTTTTGAAAACATCAGGGCTGCTGGGGGCAAGATGTG 594

Qy        186 ----------------------------------------------PheLysMetAspGl 190
Db        595 CTGGGCACCAAAGAGCATAGAGTGCCGGGCGGAGAACTACCCCGAGGTAAGCATCGACCA 654

Qy        190 uAlaSerAlaGlnLeuLeuAlaTyrLysGlu--------------LysGlyHisSerGl 205
Db        655 GGTCGGGCAGGTGCTGACCTGCAGCCTGGAGACGGGGCTGACCTGCAAGAACGAAGACCA 714

Qy        205 nSerSerGlnPheSerSer------AspGlnGluIleAlaHisLeuLeuProGluAsnVa 223
Db        715 GACAGGCAGGTTCAACATGTGCTTCAACTACAACGTGCGTGTGCTTTGCTGTGACGACTA 774

Qy        223 lSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAlaThrProLy 243
Db        775 CAGCCACTGCCCCAGTACCCCAGCCACCAGCTCCACGGCCACGCCCTCCTCAACTCCGGG 834

Qy        243 sProAlaThrLeuLeu------ProThrAsnAlaSerValThrProSerGlyThrSerGl 261
Db        835 GACGACCTGGATCCTCACAAAGCCGACCACAACAGCCACTACGACTGCGTCCACT----- 889

Qy        261 nProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThrTh 281
Db        890 ----------GGATCCACGGCCACCCCGACCTCCACCCTGAGAACAGCTCCCCCTCCCAA 939

Qy        281 rLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThrAl 301
Db        940 AGTGCTGACCACCACG--------------------------------GCCACCACACC 966

Qy        301 aValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIlePr 321
Db        967 CACAGTCACCAGCTCCAAAGCCACTCCCTCCTCCAGTCCAGGGACTGCAACCGCCCTTCC 1026

Qy        321 oPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAlaLe 341
Db       1027 AGCACTGAGAAGCACAGCCACCACA----------------------CCCACAGCTAC 1062

Qy        341 uSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArgGl 361
Db       1063 CAGCGTTACACCCATCCCCTCTTCCTCCCTGGGCACCACCTGGACCCGCCTATCACAGAC 1122

Qy        361 uAlaSerPro------------GlySerSerSerGlnGlySerValProGluAsnGlnTy 377
Db       1123 CACCACACCCACGGCCACCATGTCCACAGCCACACCCTCCTCCACTCCAGAGACTGCCCA 1182

Qy        377 r 377
Db       1183 C 1183
```

RESULT 9
US-09-241-581B-5
; Sequence 5, Application US/09241581B
; Patent No. 6350859
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center

```
;                    1201 West Peachtree Street
;               CITY: Atlanta
;               STATE: Georgia
;               COUNTRY: USA
;               ZIP: 30309-3450
;          COMPUTER READABLE FORM:
;               MEDIUM TYPE: Floppy disk
;               COMPUTER: IBM PC compatible
;               OPERATING SYSTEM: PC-DOS/MS-DOS
;               SOFTWARE: PatentIn Release #1.0, Version #1.25
;          CURRENT APPLICATION DATA:
;               APPLICATION NUMBER: US/09/241,581B
;               FILING DATE: 02-Feb-1999
;               CLASSIFICATION: <Unknown>
;          ATTORNEY/AGENT INFORMATION:
;               NAME: Pabst, Patrea L.
;               REGISTRATION NUMBER: 31,284
;               REFERENCE/DOCKET NUMBER: MIT6620
;          TELECOMMUNICATION INFORMATION:
;               TELEPHONE: (404) 873-8794
;               TELEFAX: (404) 873-8795
;     INFORMATION FOR SEQ ID NO: 5:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 2032 base pairs
;               TYPE: nucleic acid
;               STRANDEDNESS: double
;               TOPOLOGY: linear
;          MOLECULE TYPE: cDNA
;          HYPOTHETICAL: NO
;          ANTI-SENSE: NO
;          FEATURE:
;               NAME/KEY:  misc. feature
;               LOCATION:  40..1926
;               OTHER INFORMATION:   /Function = "Nucleotides 40 through
;               1926 encode the amino acid sequence
;               for the Drosophila Melanogaster
;               Scavenger Receptor Class CI."
;          SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-241-581B-5

Alignment Scores:
Pred. No.:                9.8e-05        Length:          2032
Score:                    148.00         Matches:         69
Percent Similarity:       36.05%         Conservative:    37
Best Local Similarity:    23.47%         Mismatches:      108
Query Match:              6.69%          Indels:          80
DB:                       3              Gaps:            9

US-10-735-014-83 (1-431) x US-09-241-581B-5 (1-2032)

Qy        147 SerGlnAlaValThrProLeuAla-HisHisHisThrAspTyrSerLysProThrAspIl 166
              |||   |||   |||   |||||| ||||||   |||:::   |||         |||
Db        965 AGTGTGGCACAAACGGATTTAGCACCACCACAGAACCAACGGCTCC---------GACAG 1015

Qy        166 eSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAspHisLeuGluLysLeuPh 186
                  |||   |||         ::::::                  :::||||||||
Db       1016 GCAGCAACGAGCAACCACTGGTCTACGATAT-----------------GATAAGTTGTT 1057

Qy        186 eLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGluLysGlyHisSerGlnSe 206
              |:::                        |||   |||   ::::::   :::|||
Db       1058 CAGGTCGATGCGGAACATCAATGTCGGCCTCCAATATAACCAACAATGGTATAGTCATGG 1117

Qy        206 rSer------------------GlnPheSerSerAsp---------------------- 212
                                     |||      |||
Db       1118 GATGTGGATGTAATGACGAGTGCCTTTCGGATGAGACTTGTTGCCTAAACTATTTGGAGG 1177

Qy        213 -------GlnGluIleAlaHis-LeuLeuProGluAsnValSerAlaLeuProAlaThrV 230
                  :::      ||||||          :::::::::|||:::||||||   ||||
Db       1178 AGTGCACAAAGGAGCTGCTCACCACGACCGAGGATGATATTAGTTCCCTGCCCCCAACGG 1237

Qy        230 alAlaValAlaSerProHisThr--------------------------------ThrS 239
              ||          |||      |||                                |||:
Db       1238 TCACATCAACAAGCACAAGCACTACGAGGAAGTCAACAACAACAACAACCACAAGCACGA 1297

Qy        239 erAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyT 259
              ::   |||               |||       ||||||       :::   |||       |
Db       1298 CTACTACAAGTACAACAACAACTAAAAGGCCAACCACAACCACAACAACAACAAAGGCCA 1357

Qy        259 hrSerGlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProP 279
              ||:::     :::      ||||||      |||   ||||||   |||:::      |
Db       1358 CAACTACAAAGCGAACAACAACCACTAAAAAACCGACAACAACTTCAACAACGCCGAAGC 1417

Qy        279 roThrThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaT 299
              ||||||||      ||||||                        :::|||          :::|
Db       1418 CAACAACAACGACTTCAACCACACCAAAGTCTACAACTTCTACAACGTCTACAACTTCAA 1477

Qy        299 hrThrAlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluT 319
              |||||         |||||||||              |||      |||
Db       1478 CAACACCAACGACAACAACTACAATAAATGTGTTTACAACAAAGAAA------------ 1524

Qy        319 hrIleProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProT 339
                                    :::   :::   :::   |||   :::          |
Db       1525 -------------------ACAACAATAATGATCCCTACTTCCAGTACCGAAAAGACTA 1564

Qy        339 hrAlaLeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrp---- 357
              ||   :::            :::   :::                |||      :::|||
Db       1565 CAGGCATC------------ATCACCACCATGAAGACACGCAAGCGCATCACTTGGAACG 1612

Qy        358 ----------------GluGlyArgGluAlaSerProGlySerSerSerGlnGlySerV 372
                             ||||||         :::   ||||||:::         ::::
Db       1613 TTGATCCTCAGGACATCGAGGGTCACATGGACACGAGCGGAAGTACCCCCAATCCAGCTT 1672

Qy        372 alProGluAsnGlnTyrGlyLeuProPheGluLysTrpLeuLeuIleGlySerLeuLeuP 392
              ::
Db       1673 TAGTA---------------------------------------------------- 1677

Qy        392 heGlyValLeuPheLeuValIleGlyLeuValLeuLeu 404
                    ||||||:::|||::::::|||:::||||||:::
Db       1678 -----GTACTTTACCTGCTACTCGGCATTGTTCTGGTG 1710

RESULT 10
US-08-265-428-5
; Sequence 5, Application US/08265428
; Patent No. 6429289
;  GENERAL INFORMATION:
;    APPLICANT:  Krieger, Monty
;    TITLE OF INVENTION:  Class BI Scavenger Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  1100 Peachtree Street, Suite 2800
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30309-4530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,428
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  MIT6620
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (404) 815-6508
;      TELEFAX:  (404) 815-6555
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2032 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
```

```
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  misc. feature
;      LOCATION:  40..1926
;      OTHER INFORMATION:  /Function = "Nucleotides 40 through 1926 encode the amino aci
US-08-265-428-5

Alignment Scores:
Pred. No.:              9.8e-05       Length:        2032
Score:                  148.00        Matches:       69
Percent Similarity:     36.05%        Conservative:  37
Best Local Similarity:  23.47%        Mismatches:    108
Query Match:            6.69%         Indels:        80
DB:                     3             Gaps:          9

US-10-735-014-83 (1-431) x US-08-265-428-5 (1-2032)

Qy        147 SerGlnAlaValThrProLeuAla-HisHisHisThrAspTyrSerLysProThrAspIl 166
              |||   |||   |||   |||||| ||||||   |||:::   |||          |||
Db        965 AGTGTGGCACAAACGGATTTAGCACCACCACAGAACCAACGGCTCC---------GACAG 1015

Qy        166 eSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAspHisLeuGluLysLeuPh 186
              |||   |||         ::::::                   :::||||||||
Db       1016 GCAGCAACGAGCAACCACTGGTCTACGATAT-----------------GATAAGTTGTT 1057

Qy        186 eLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGluLysGlyHisSerGlnSe 206
              |:::                        |||   |||   ::::::   :::|||
Db       1058 CAGGTCGATGCGGAACATCAATGTCGGCCTCCAATATAACCAACAATGGTATAGTCATGG 1117

Qy        206 rSer------------------GlnPheSerSerAsp---------------------- 212
                                    |||      |||
Db       1118 GATGTGGATGTAATGACGAGTGCCTTTCGGATGAGACTTGTTGCCTAAACTATTTGGAGG 1177

Qy        213 -------GlnGluIleAlaHis-LeuLeuProGluAsnValSerAlaLeuProAlaThrV 230
                  :::      ||||||         :::::::::|||:::||||||   ||||
Db       1178 AGTGCACAAAGGAGCTGCTCACCACGACCGAGGATGATATTAGTTCCCTGCCCCCAACGG 1237

Qy        230 alAlaValAlaSerProHisThr--------------------------------ThrS 239
              ||         |||      |||                                  |||:
Db       1238 TCACATCAACAAGCACAAGCACTACGAGGAAGTCAACAACAACAACAACCACAAGCACGA 1297

Qy        239 erAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyT 259
              ::   |||           |||      ||||||      :::   |||          |
Db       1298 CTACTACAAGTACAACAACAACTAAAAGGCCAACCACAACCACAACAACAACAAAGGCCA 1357

Qy        259 hrSerGlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProP 279
              ||:::      :::      ||||||      |||   ||||||   |||:::      |
Db       1358 CAACTACAAAGCGAACAACAACCACTAAAAAACCGACAACAACTTCAACAACGCCGAAGC 1417

Qy        279 roThrThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaT 299
              ||||||||      ||||||                  :::|||           :::|
Db       1418 CAACAACAACGACTTCAACCACACCAAAGTCTACAACTTCTACAACGTCTACAACTTCAA 1477

Qy        299 hrThrAlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluT 319
              |||||          |||||||||           |||      |||
Db       1478 CAACACCAACGACAACAACTACAATAAATGTGTTTACAACAAAGAAA------------- 1524

Qy        319 hrIleProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProT 339
                          :::   :::   :::   |||   :::                  |
Db       1525 -------------------ACAACAATAATGATCCCTACTTCCAGTACCGAAAAGACTA 1564

Qy        339 hrAlaLeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrp---- 357
              ||   :::            :::   :::           |||      :::|||
Db       1565 CAGGCATC-----------ATCACCACCATGAAGACACGCAAGCGCATCACTTGGAACG 1612

Qy        358 ----------------GluGlyArgGluAlaSerProGlySerSerSerGlnGlySerV 372
                          ||||||       :::   ||||||:::      ::::
Db       1613 TTGATCCTCAGGACATCGAGGGTCACATGGACACGAGCGGAAGTACCCCCAATCCAGCTT 1672

Qy        372 alProGluAsnGlnTyrGlyLeuProPheGluLysTrpLeuLeuIleGlySerLeuLeuP 392
                ::
Db       1673 TAGTA---------------------------------------------------- 1677

Qy        392 heGlyValLeuPheLeuValIleGlyLeuValLeuLeu 404
                  ||||||:::|||:::::::|||:::||||||:::
Db       1678 -----GTACTTTACCTGCTACTCGGCATTGTTCTGGTG 1710

RESULT 11
PCT-US95-07721-5
; Sequence 5, Application PC/TUS9507721
;  GENERAL INFORMATION:
;    APPLICANT:  Massachusetts Institute of Technology
;    TITLE OF INVENTION:  Class BI and CI Scavenger Receptors
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  2800 One Atlantic Center
;      STREET:  1201 West Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30309-3450
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/07721
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  MIT6620
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (404) 873-8794
;      TELEFAX:  (404) 873-8795
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2032 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  misc. feature
;      LOCATION:  40..1926
;      OTHER INFORMATION:  /Function = "Nucleotides 40 through
;      OTHER INFORMATION:  1926 encode the amino acid sequence
;      OTHER INFORMATION:  for the Drosophila Melanogaster
;      OTHER INFORMATION:  Scavenger Receptor Class CI."
PCT-US95-07721-5

Alignment Scores:
Pred. No.:              9.8e-05       Length:        2032
Score:                  148.00        Matches:       69
Percent Similarity:     36.05%        Conservative:  37
Best Local Similarity:  23.47%        Mismatches:    108
Query Match:            6.69%         Indels:        80
DB:                     5             Gaps:          9

US-10-735-014-83 (1-431) x PCT-US95-07721-5 (1-2032)

Qy        147 SerGlnAlaValThrProLeuAla-HisHisHisThrAspTyrSerLysProThrAspIl 166
              |||   |||   |||   |||||| ||||||   |||:::   |||          |||
Db        965 AGTGTGGCACAAACGGATTTAGCACCACCACAGAACCAACGGCTCC---------GACAG 1015

Qy        166 eSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAspHisLeuGluLysLeuPh 186
              |||   |||         ::::::                   :::||||||||
Db       1016 GCAGCAACGAGCAACCACTGGTCTACGATAT-----------------GATAAGTTGTT 1057
```

```
Qy        186 eLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGluLysGlyHisSerGlnSe 206
              |:::                        |||   |||   ::::::   :::|||
Db       1058 CAGGTCGATGCGGAACATCAATGTCGGCCTCCAATATAACCAACAATGGTATAGTCATGG 1117

Qy        206 rSer-----------------GlnPheSerSerAsp---------------------- 212
                                  |||       |||
Db       1118 GATGTGGATGTAATGACGAGTGCCTTTCGGATGAGACTTGTTGCCTAAACTATTTGGAGG 1177

Qy        213 -------GlnGluIleAlaHis-LeuLeuProGluAsnValSerAlaLeuProAlaThrV 230
                  :::      ||||||          :::::::::|||:::||||||   ||||
Db       1178 AGTGCACAAAGGAGCTGCTCACCACGACCGAGGATGATATTAGTTCCCTGCCCCCAACGG 1237

Qy        230 alAlaValAlaSerProHisThr--------------------------------ThrS 239
              ||       |||      |||                                   |||:
Db       1238 TCACATCAACAAGCACAAGCACTACGAGGAAGTCAACAACAACAACAACCACAAGCACGA 1297

Qy        239 erAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyT 259
              ::   |||             |||      ||||||      :::   |||          |
Db       1298 CTACTACAAGTACAACAACAACTAAAAGGCCAACCACAACCACAACAACAACAAAGGCCA 1357

Qy        259 hrSerGlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProP 279
              ||:::     :::      ||||||      |||   ||||||   |||:::      |
Db       1358 CAACTACAAAGCGAACAACAACCACTAAAAAACCGACAACAACTTCAACAACGCCGAAGC 1417

Qy        279 roThrThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaT 299
              ||||||||      ||||||                  :::|||            :::|
Db       1418 CAACAACAACGACTTCAACCACACCAAAGTCTACAACTTCTACAACGTCTACAACTTCAA 1477

Qy        299 hrThrAlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluT 319
              |||||         |||||||||             |||      |||
Db       1478 CAACACCAACGACAACAACTACAATAAATGTGTTTACAACAAAGAAA------------ 1524

Qy        319 hrIleProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProT 339
                          :::   :::   :::   |||   :::                  |
Db       1525 -------------------ACAACAATAATGATCCCTACTTCCAGTACCGAAAAGACTA 1564

Qy        339 hrAlaLeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrp---- 357
              ||   :::            :::   :::           |||      :::|||
Db       1565 CAGGCATC-----------ATCACCACCATGAAGACACGCAAGCGCATCACTTGGAACG 1612

Qy        358 -----------------GluGlyArgGluAlaSerProGlySerSerSerGlnGlySerV 372
                              |||||         :::   ||||||:::        ::::
Db       1613 TTGATCCTCAGGACATCGAGGGTCACATGGACACGAGCGGAAGTACCCCCAATCCAGCTT 1672

Qy        372 alProGluAsnGlnTyrGlyLeuProPheGluLysTrpLeuLeuIleGlySerLeuLeuP 392
              ::
Db       1673 TAGTA---------------------------------------------------- 1677

Qy        392 heGlyValLeuPheLeuValIleGlyLeuValLeuLeu 404
                   ||||||:::|||::::::|||:::||||||:::
Db       1678 -----GTACTTTACCTGCTACTCGGCATTGTTCTGGTG 1710

RESULT 12
US-09-949-016-12147/c
; Sequence 12147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12147
;  LENGTH: 767677
;  TYPE: DNA
;  ORGANISM: Human
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)...(767677)
;  OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12147

Alignment Scores:
Pred. No.:              5.74          Length:          767677
Score:                  146.00        Matches:         81
Percent Similarity:     37.36%        Conservative:    21
Best Local Similarity:  29.67%        Mismatches:      120
Query Match:            6.60%         Indels:          51
DB:                     4             Gaps:            14

US-10-735-014-83 (1-431) x US-09-949-016-12147 (1-767677)

Qy         88 LysThrAlaArgGlnProAsnCysTyr---LeuPhePheCysProAsnGluGluAlaCys 106
              |||      |||  |||  |||                 |||      :::   ||||||
Db     753296 AAGGAAGGCCGCTGGCCACCATGTACCCCACAGACACTGTGCAGCCCACAGCCAGCATGC 753237

Qy        107 ---ProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIleThrAspPheProSer 125
                 |||      |||          :::|||:::         |||      |||
Db     753236 ACCCCACACACCCCA-----------CTATCACACACCCCACACACCCCACAGCCACCA 753189

Qy        126 LeuThrArgAsnLeuPro-SerGlnGluLeuProGlnGluAspSerLeuLeuHisGlyGl 145
                 |||         ||| |||      |||              |||
Db     753188 CACACCCCACGCACCCCACAGCCATCACACACCCCACAGCCACCACACAACCCACAGCCA 753129

Qy        145 nPheSerGln---------------AlaValThrProLeuAlaHis-------------- 155
                 :::                        ||||||   :::|||
Db     753128 CCACGCATCCCACAGCCACCACGCACCCCACACACCCCACAGCCATCACACACCCCACGG 753069

Qy        156 -HisHisThrAspTyrSerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLy 175
               |||||||||   :::|||      |||      |||              |||
Db     753068 GCACCACACACCCCACAGCCACCACACACCCCACAGCCACCACACACCCCACAGCCACCA 753009

Qy        175 sPheGlySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLe 195
                    |||  |||
Db     753008 CACAACCCACAGCCACCACACAACC---------------------------------- 752984

Qy        195 uLeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIl 215
                                  ||||||      :::      |||
Db     752983 ----------------------CACAGCCACCATGCACCCCACAGCCAGCACGCACCCCA 752946

Qy        215 eAlaHisLeuLeuProGluAsnValSerAlaLeu-ProAlaThrVal---AlaValAlaS 234
               :::|||      |||  :::      |||         ||||||      ||||
Db     752945 CAGCCACCACGCACCCCACAGCCAGCACGCATCCCACAGCCACCACACACCCCACAGCCA 752886

Qy        234 erProHisThrThrSerAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSerV 254
               ||   |||            |||         ||||||      ||||||   ||||||:
Db     752885 GCACGCACCCCATGGGCACCACGCACCCCACAGCCACCACACACCCCACA---GCCAGCA 752829

Qy        254 alThrProSerGlyThrSerGlnProGlnLeuAlaThrThrAlaProProValThr---- 272
               ::   |||   ||||||:::   |||      |||||||||   |||      |||
Db     752828 TGCACCCCATGGGCACCACGCACCCC---ACAGCCACCACACAACCCACAGCCACCACGC 752772

Qy        273 -----ThrValThrSerGlnProProThrThrLeuIleSerThrValPheThrArgAlaA 291
                   |||   |||:::||||||      |||         |||      |||:::
Db     752771 ACCCCACAGCCACCACACAACCCACGGCCACCACACACCCCACAGCCAGCACCCAACCCA 752712

Qy        291 laAlaThrLeuGlnAlaMetAlaThrThrAlaValLeuThrThrThrPheGlnAlaProT 311
               |||             |||  ||||||           ||||||:::      ||||
Db     752711 CAGCTGGCACACACCCCATGACCACCACACACTCCACAGCCACCACATAC------CCTA 752658

Qy        311 hrAspSerLysGlySerLeuGluThrIle-ProPheThrGluIleSerAsnLeuThrLeu 330
               ||         |||::::::   :::::: |||         :::   :::||||||
Db     752657 CA---------GGAGCCATGCACTCTATGGCCACTGCACACCCTGTGGTCACTGACCACA 752607

Qy        331 Asn---ThrGlyAsnValTyrAsnProThrAla 340
                  :::   |||      ||||||   |||||||||
```

```
Db     752606 CACCCCACAGCCACCGTGTAC---CCCACGGCC 752577

RESULT 13
US-09-949-016-17361/c
; Sequence 17361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17361
;   LENGTH: 767677
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(767677)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361

Alignment Scores:
Pred. No.:              5.74          Length:         767677
Score:                  146.00        Matches:        81
Percent Similarity:     37.36%        Conservative:   21
Best Local Similarity:  29.67%        Mismatches:     120
Query Match:            6.60%         Indels:         51
DB:                     4             Gaps:           14

US-10-735-014-83 (1-431) x US-09-949-016-17361 (1-767677)

Qy         88 LysThrAlaArgGlnProAsnCysTyr---LeuPhePheCysProAsnGluGluAlaCys 106
              |||      |||   |||   |||                |||      :::   ||||||
Db     753296 AAGGAAGGCCGCTGGCCACCATGTACCCCACAGACACTGTGCAGCCCACAGCCAGCATGC 753237

Qy        107 ---ProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIleThrAspPheProSer 125
                 |||      |||           :::|||:::         |||      |||
Db     753236 ACCCCACACACCCCA-----------CTATCACACACCCCACACACCCCACAGCCACCA 753189

Qy        126 LeuThrArgAsnLeuPro-SerGlnGluLeuProGlnGluAspSerLeuLeuHisGlyGl 145
                 |||         ||| |||         |||                  |||
Db     753188 CACACCCCACGCACCCCACAGCCATCACACACCCCACAGCCACCACACAACCCACAGCCA 753129

Qy        145 nPheSerGln---------------AlaValThrProLeuAlaHis-------------- 155
                 :::                        ||||||   :::|||
Db     753128 CCACGCATCCCACAGCCACCACGCACCCCACACACCCCACAGCCATCACACACCCCACGG 753069

Qy        156 -HisHisThrAspTyrSerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLy 175
               |||||||||   :::|||      |||      |||                  |||
Db     753068 GCACCACACACCCCACAGCCACCACACACCCCACAGCCACCACACACCCCACAGCCACCA 753009

Qy        175 sPheGlySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLe 195
                    |||  |||
Db     753008 CACAACCCACAGCCACCACACAACC---------------------------------- 752984

Qy        195 uLeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIl 215
                                  ||||||      :::      |||
Db     752983 ----------------------CACAGCCACCATGCACCCCACAGCCAGCACGCACCCCA 752946

Qy        215 eAlaHisLeuLeuProGluAsnValSerAlaLeu-ProAlaThrVal---AlaValAlaS 234
               :::|||      |||   :::      |||       ||||||             ||||
Db     752945 CAGCCACCACGCACCCCACAGCCAGCACGCATCCCACAGCCACCACACACCCCACAGCCA 752886

Qy        234 erProHisThrThrSerAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSerV 254
               ||   |||              |||          ||||||      ||||||   ||||||:
Db     752885 GCACGCACCCCATGGGCACCACGCACCCCACAGCCACCACACACCCCACA---GCCAGCA 752829

Qy        254 alThrProSerGlyThrSerGlnProGlnLeuAlaThrThrAlaProProValThr---- 272
               ::   |||   ||||||:::   |||      |||||||||   |||      |||
Db     752828 TGCACCCCATGGGCACCACGCACCCC---ACAGCCACCACACAACCCACAGCCACCACGC 752772

Qy        273 -----ThrValThrSerGlnProProThrThrLeuIleSerThrValPheThrArgAlaA 291
                    |||   |||:::||||||      |||        |||      |||:::
Db     752771 ACCCCACAGCCACCACACAACCCACGGCCACCACACACCCCACAGCCAGCACCCAACCCA 752712

Qy        291 laAlaThrLeuGlnAlaMetAlaThrThrAlaValLeuThrThrThrPheGlnAlaProT 311
               |||            |||   ||||||            ||||||:::      ||||
Db     752711 CAGCTGGCACACACCCCATGACCACCACACACTCCACAGCCACCACATAC------CCTA 752658

Qy        311 hrAspSerLysGlySerLeuGluThrIle-ProPheThrGluIleSerAsnLeuThrLeu 330
               ||        |||::::::   :::::: |||        :::   :::||||||
Db     752657 CA---------GGAGCCATGCACTCTATGGCCACTGCACACCCTGTGGTCACTGACCACA 752607

Qy        331 Asn---ThrGlyAsnValTyrAsnProThrAla 340
                  :::   |||      ||||||   |||||||||
Db     752606 CACCCCACAGCCACCGTGTAC---CCCACGGCC 752577

RESULT 14
US-09-370-838-158/c
; Sequence 158, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
;  APPLICANT: Reed, Steven G.
;  APPLICANT: Lodes, Michael J.
;  APPLICANT: Mohamath, Roadoh
;  APPLICANT: Secrist, Heather
;  TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
;  TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.475C1
;  CURRENT APPLICATION NUMBER: US/09/370,838
;  CURRENT FILING DATE: 1999-08-09
;  EARLIER APPLICATION NUMBER: US 09/285,323
;  EARLIER FILING DATE: 1999-04-02
;  NUMBER OF SEQ ID NOS: 289
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 158
;   LENGTH: 2114
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-370-838-158

Alignment Scores:
Pred. No.:              0.00019       Length:         2114
Score:                  145.50        Matches:        63
Percent Similarity:     40.74%        Conservative:   25
Best Local Similarity:  29.17%        Mismatches:     66
Query Match:            6.58%         Indels:         62
DB:                     3             Gaps:           9

US-10-735-014-83 (1-431) x US-09-370-838-158 (1-2114)

Qy        204 SerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuProGluAsnVal 223
              |||::::::::::   |||||||||                        |||
Db       1999 TCCAAAGCCACTCCCTTCTCCAGT-----------------------CCAGGGACTGCA 1964

Qy        224 SerAlaLeuProAlaThrValAlaValAla---SerProHisThrThrSerAlaThrPro 242
              :::||||||||||||      :::   |||   :::|||      ||||||   |||
Db       1963 ACCGCCCTTCCAGCACTGAGAAGCACAGCCACCACACCCACAGCTACCAGCTTTACAGCC 1904

Qy        243 LysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSerGlnPro 262
                 |||::::::   |||                              ||||||:::
Db       1903 ATCCCCTCCTCCTCCCTG-------------------------GGCACCACCTGGACC 1871

Qy        263 GlnLeuAlaThrThrAlaProProValThrThrVal--------------ThrSerGln 277
              :::|||:::   |||      |||      |||:::                 :::|||
Db       1870 CGCCTATCACAGACCACCACACCCACGGCCACCATGTCCACAGCCACACCCTCCTCCACT 1811
```

```
Qy       278 ProProThrThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMet 297
Db      1810 CCAGAGACTGCCCACACCTCCACAGTGCTTACCACCACGGCCACCACAACCAGGGCCACC 1751

Qy       298 Ala-------------------------------------ThrThrAlaValLeuThr 304
Db      1750 GGCTCTGTGGCCACCCCCTCTTCCACCCCAGGAACAGCTCACACTACCAAAGTGCCGACT 1691

Qy       305 ThrThrPheGln------------AlaProThrAspSerLysGlySerLeuGluThrIle 320
Db      1690 ACCACAACCACGGGCTTCACAGTCACCCCCTCCTTCAGCCCAGGGACGGCACGCACGCCT 1631

Qy       321 ProPheThrGluIleSerAsnLeuThrLeuAsnThr------------------------ 332
Db      1630 CCA---GTGTGGATCAGCACAACCACCACACCCACAACCAGTGGCTTCACGGTGACCCCC 1574

Qy       333 ------------GlyAsnValTyrAsnProThrAlaLeuSerMetSerAsnValGluSer 348
Db      1573 TCCTCCGTCCCGGGGACCACCCACACCCCCACAGTGCTGACCACCACCACCACAACTGTG 1514

Qy       349 SerThrMetAsnLysThrAlaSerTrpGluGlyArgGluAlaSerProGlySerSerSer 368
Db      1513 GCCACT----------------------GGTTCTATGGCAACACCCTCCTCTAGCACA 1478

Qy       369 GlnGlySer-ValProGluAsnGlnTyrGlyLeuProPheGluLys 383
Db      1477 CAGACCAGTGGTACCTCGTGCCGAATTCGGCACCAGGGCTGACAAG 1432
```

RESULT 15
US-09-854-133-158/c
; Sequence 158, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 2114
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-854-133-158

Alignment Scores:

Pred. No.:	0.00019	Length:	2114
Score:	145.50	Matches:	63
Percent Similarity:	40.74%	Conservative:	25
Best Local Similarity:	29.17%	Mismatches:	66
Query Match:	6.58%	Indels:	62
DB:	4	Gaps:	9

US-10-735-014-83 (1-431) x US-09-854-133-158 (1-2114)

```
Qy       204 SerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuProGluAsnVal 223
Db      1999 TCCAAAGCCACTCCCTTCTCCAGT----------------------CCAGGGACTGCA 1964

Qy       224 SerAlaLeuProAlaThrValAlaValAla---SerProHisThrThrSerAlaThrPro 242
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Qy       243 LysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSerGlnPro 262
Db      1903 ATCCCCTCCTCCTCCCTG------------------------GGCACCACCTGGACC 1871

Qy       263 GlnLeuAlaThrThrAlaProProValThrThrVal--------------ThrSerGln 277
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Qy       278 ProProThrThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMet 297
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Qy       321 ProPheThrGluIleSerAsnLeuThrLeuAsnThr------------------------ 332
Db      1630 CCA---GTGTGGATCAGCACAACCACCACACCCACAACCAGTGGCTTCACGGTGACCCCC 1574

Qy       333 ------------GlyAsnValTyrAsnProThrAlaLeuSerMetSerAsnValGluSer 348
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Qy       349 SerThrMetAsnLysThrAlaSerTrpGluGlyArgGluAlaSerProGlySerSerSer 368
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Search completed: April 27, 2005, 01:07:23
Job time : 575 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 26, 2005, 23:55:07 ; Search time 644 Seconds
(without alignments)
4063.079 Million cell updates/sec

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Perfect score: 2211
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Ygapop 10.0 , Ygapext 0.5
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Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2211	100.0	2284	9	US-09-866-028-82	Sequence 82, Appl
2	2211	100.0	2284	9	US-09-989-722-514	Sequence 514, App
3	2211	100.0	2284	9	US-09-989-723-514	Sequence 514, App
4	2211	100.0	2284	9	US-09-989-279-514	Sequence 514, App
5	2211	100.0	2284	9	US-09-989-727-514	Sequence 514, App
6	2211	100.0	2284	9	US-09-944-449-82	Sequence 82, Appl
7	2211	100.0	2284	9	US-09-989-731-514	Sequence 514, App
8	2211	100.0	2284	9	US-09-944-457-82	Sequence 82, Appl
9	2211	100.0	2284	9	US-09-989-732-514	Sequence 514, App
10	2211	100.0	2284	9	US-09-991-073-514	Sequence 514, App
11	2211	100.0	2284	9	US-09-945-587-82	Sequence 82, Appl
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13	2211	100.0	2284	9	US-09-991-163-514	Sequence 514, App
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15	2211	100.0	2284	9	US-09-944-396-82	Sequence 82, Appl
16	2211	100.0	2284	9	US-09-993-604-514	Sequence 514, App
17	2211	100.0	2284	9	US-09-990-456-514	Sequence 514, App
18	2211	100.0	2284	9	US-09-944-432-82	Sequence 82, Appl
19	2211	100.0	2284	9	US-09-943-762-82	Sequence 82, Appl
20	2211	100.0	2284	9	US-09-944-654-82	Sequence 82, Appl
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23	2211	100.0	2284	9	US-09-944-413-82	Sequence 82, Appl
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ALIGNMENTS

RESULT 1
US-09-866-028-82
; Sequence 82, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel

```
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/866,028
;  CURRENT FILING DATE:  2001-05-25
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 82
;   LENGTH: 2284
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-866-028-82

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RESULT 2
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; Patent No. US20020072067A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C63
;  CURRENT APPLICATION NUMBER: US/09/989,722
;  CURRENT FILING DATE:  2001-11-19
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; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
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; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-04-28
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;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.:              1.47e-211       Length:         2284
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Percent Similarity:     100.00%         Conservative:   0
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US-10-735-014-83 (1-431) x US-09-989-722-514 (1-2284)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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RESULT 3
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; Sequence 514, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
```

; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
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; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.:                1.47e-211      Length:          2284
Score:                    2211.00        Matches:         431
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       9              Gaps:            0

US-10-735-014-83 (1-431) x US-09-989-723-514 (1-2284)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

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Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

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Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

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Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 4
US-09-989-279-514
; Sequence 514, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
```

; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

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Score:                    2211.00        Matches:         431
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Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
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US-10-735-014-83 (1-431) x US-09-989-279-514 (1-2284)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

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Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 5
US-09-989-727-514
; Sequence 514, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
```

; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
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; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
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; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
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; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435

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;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090444
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090445
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090472
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090535
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090540
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090542
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090557
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090676
;  PRIOR FILING DATE: 1998-06-25
;  PRIOR APPLICATION NUMBER: 60/090678
;  PRIOR FILING DATE: 1998-06-25
;  PRIOR APPLICATION NUMBER: 60/090690
;  PRIOR FILING DATE: 1998-06-25
;  PRIOR APPLICATION NUMBER: 60/090694
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;  PRIOR APPLICATION NUMBER: 60/090695
;  PRIOR FILING DATE: 1998-06-25
;  PRIOR APPLICATION NUMBER: 60/090696
;  PRIOR FILING DATE: 1998-06-25
;  PRIOR APPLICATION NUMBER: 60/090862
;  PRIOR FILING DATE: 1998-06-26
;  PRIOR APPLICATION NUMBER: 60/090863
;  PRIOR FILING DATE: 1998-06-26
;  PRIOR APPLICATION NUMBER: 60/091360
;  PRIOR FILING DATE: 1998-07-01
;  PRIOR APPLICATION NUMBER: 60/091478
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: 60/091544
;  PRIOR FILING DATE: 1998-07-01
;  PRIOR APPLICATION NUMBER: 60/091519
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: 60/091626
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: 60/091633
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: 60/091978
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/091982
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.:              1.47e-211       Length:         2284
Score:                  2211.00         Matches:        431
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-10-735-014-83 (1-431) x US-09-989-727-514 (1-2284)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 6
US-09-944-449-82
; Sequence 82, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,449
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,694
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,702
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/069,873
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: December1, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 82
;   LENGTH: 2284
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-944-449-82

Alignment Scores:
Pred. No.:              1.47e-211       Length:         2284
Score:                  2211.00         Matches:        431
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
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US-10-735-014-83 (1-431) x US-09-944-449-82 (1-2284)

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Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

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Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 7
US-09-989-731-514
; Sequence 514, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION:  Acids Encoding the Same
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE:  2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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US-10-735-014-83 (1-431) x US-09-989-731-514 (1-2284)

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Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Qy       101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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; Patent No. US20020110859A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,457
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
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;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
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;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
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;  PRIOR APPLICATION NUMBER: 60/113,296
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;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
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;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
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;  PRIOR APPLICATION NUMBER: 09/254,311
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;  PRIOR FILING DATE: September 15, 1999
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;  PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
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;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
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;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
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;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-944-457-82

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Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
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Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 9
US-09-989-732-514
; Sequence 514, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
```

; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity:	100.00%	Mismatches:	0
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US-10-735-014-83 (1-431) x US-09-989-732-514 (1-2284)

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Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

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Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

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Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

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RESULT 10
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; Sequence 514, Application US/09991073
; Patent No. US20020127576A1

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C15
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; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	1.47e-211	Length:	2284
Score:	2211.00	Matches:	431
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-735-014-83 (1-431) x US-09-991-073-514 (1-2284)

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Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485
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Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 11
US-09-945-587-82
; Sequence 82, Application US/09945587
; Patent No. US20020127643A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/945,587
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,694
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,702
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/069,873
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: December1, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
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;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-945-587-82

Alignment Scores:
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Query Match:              100.00%        Indels:          0
DB:                       9              Gaps:            0

US-10-735-014-83 (1-431) x US-09-945-587-82 (1-2284)

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Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

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Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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RESULT 12
US-09-990-442-514
; Sequence 514, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C8
;  CURRENT APPLICATION NUMBER: US/09/990,442
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/065186
;  PRIOR FILING DATE: 1997-11-12
;  PRIOR APPLICATION NUMBER: 60/065311
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/066770
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/075945
;  PRIOR FILING DATE: 1998-02-25
;  PRIOR APPLICATION NUMBER: 60/078910
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/083322
;  PRIOR FILING DATE: 1998-04-28
;  PRIOR APPLICATION NUMBER: 60/084600
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/087106
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;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: 60/088026
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;  PRIOR APPLICATION NUMBER: 60/088028
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; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	1.47e-211	Length:	2284
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Best Local Similarity:	100.00%	Mismatches:	0
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US-10-735-014-83 (1-431) x US-09-990-442-514 (1-2284)

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Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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RESULT 13
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; Patent No. US20020132253A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
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;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C17
;  CURRENT APPLICATION NUMBER: US/09/991,163
;  CURRENT FILING DATE:  2001-11-14
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	1.47e-211	Length:	2284
Score:	2211.00	Matches:	431
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-735-014-83 (1-431) x US-09-991-163-514 (1-2284)

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Db       526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy       121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy       141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy       161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy       181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy       201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy       221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db       886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy       241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Db       946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy       261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy       281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db      1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy       301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy       321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy       341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy       361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy       381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy       401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy       421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
             |||||||||||||||||||||||||||||||||
Db      1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518
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RESULT 14
US-09-945-015-82
; Sequence 82, Application US/09945015
; Patent No. US20020132768A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,015
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
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; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998

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;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: December1, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 82
;   LENGTH: 2284
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-945-015-82

Alignment Scores:
Pred. No.:              1.47e-211       Length:         2284
Score:                  2211.00         Matches:        431
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-10-735-014-83 (1-431) x US-09-945-015-82 (1-2284)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 645

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 15
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US-09-944-396-82
; Sequence 82, Application US/09944396
; Patent No. US20020132981A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,396
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,694
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,702
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/069,873
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: December1, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 82
;   LENGTH: 2284
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-944-396-82

Alignment Scores:
Pred. No.:              1.47e-211       Length:         2284
Score:                  2211.00         Matches:        431
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-10-735-014-83 (1-431) x US-09-944-396-82 (1-2284)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Db        226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285

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Db        286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Db        346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 525

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Db        526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        646 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Db        766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Db        946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 1065

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db       1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db       1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Db       1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Db       1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Db       1306 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1365

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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Db       1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db       1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518


Search completed: April 27, 2005, 02:27:57
Job time : 667 secs
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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 26, 2005, 22:01:01 ; Search time 3342 Seconds
(without alignments)
4908.947 Million cell updates/sec

Title: US-10-735-014-83
Perfect score: 2211
Sequence: 1 MFFGGEGSLTYTLVIICFLT.....LRRKRYSRLDYLINGIYVDI 431

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US10735014/runat_26042005_113101_7425/app_query.fasta_1.583
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10735014_@CGN_1_1_5180_@runat_26042005_113101_7425 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2211	100.0	1296	9	AY401136	AY401136 Homo sapi
2	2183	98.7	1296	9	AY401137	AY401137 Pan trogl
3	1831	82.8	1965	3	CR621081	CR621081 full-leng
4	1376	62.2	853	5	BQ424639	BQ424639 AGENCOURT
c 5	1353	61.2	884	5	BX350141	BX350141 BX350141
6	1225	55.4	1050	1	AL525434	AL525434 AL525434
7	1176.5	53.2	1245	9	AY401138	AY401138 Mus muscu
8	1164.5	52.7	2235	3	AK033526	AK033526 Mus muscu
9	1164.5	52.7	2265	3	AK018635	AK018635 Mus muscu
10	1164.5	52.7	2265	3	AK046837	AK046837 Mus muscu
11	1164.5	52.7	2286	3	AK018660	AK018660 Mus muscu
12	1164.5	52.7	2375	3	AK033557	AK033557 Mus muscu
13	1079	48.8	623	7	CV024215	CV024215 1439 Full
14	1063	48.1	753	7	CF595929	CF595929 AGENCOURT
15	1056	47.8	2227	3	AK002644	AK002644 Mus muscu
16	1038	46.9	634	6	CD695273	CD695273 EST11796
17	1019	46.1	940	2	BF683169	BF683169 602139129
18	1008	45.6	582	5	BP375799	BP375799 BP375799
19	1000	45.2	697	5	BU172626	BU172626 AGENCOURT
20	989	44.7	623	6	CD722598	CD722598 oj11f11.y
21	985	44.5	684	5	BX485439	BX485439 DKFZp686C
22	888.5	40.2	839	7	CF593691	CF593691 AGENCOURT
23	862.5	39.0	1036	1	AL549886	AL549886 AL549886
24	852	38.5	699	4	BG720669	BG720669 602692553
25	807	36.5	870	2	BF312571	BF312571 601897547
26	790	35.7	697	7	CN365249	CN365249 170005999
27	780.5	35.3	805	1	AU138119	AU138119 AU138119
28	767	34.7	668	7	CK834065	CK834065 4058249 B
29	765	34.6	447	5	BP246319	BP246319 BP246319
30	764.5	34.6	855	1	AU123305	AU123305 AU123305
31	755	34.1	602	5	BU789700	BU789700 io44h09.x
32	743.5	33.6	718	7	CK971151	CK971151 4087056 B
33	709	32.1	687	5	BX953184	BX953184 DKFZp781N
34	683	30.9	441	4	BI031052	BI031052 IL5-MT026
35	679	30.7	457	2	AW752992	AW752992 QV0-CT022
36	671	30.3	734	7	CO879641	CO879641 BovGen_07
37	670	30.3	412	4	BM820174	BM820174 K-EST0088
38	665	30.1	630	4	BM846209	BM846209 K-EST0125
39	647	29.3	667	4	BG720926	BG720926 602692181
40	645	29.2	707	7	CK974547	CK974547 4105473 B
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ALIGNMENTS

RESULT 1
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LOCUS AY401136 1296 bp DNA linear GSS 12-DEC-2003
DEFINITION Homo sapiens HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY401136
VERSION AY401136.1 GI:39757125
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1296)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1. .1296

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ORIGIN

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Score:                    2211.00       Matches:         431
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       9             Gaps:            0

US-10-735-014-83 (1-431) x AY401136 (1-1296)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 60

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 120

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Db        121 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 180

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Db        181 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 240

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        241 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 300

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Db        301 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 360

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Db        361 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 420

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 780

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Db        781 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 840

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Db        841 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 900

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1201 CTCGTCCTCCTGGGTAGAATCCTCTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1260

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db       1261 GATTATTTGATCAATGGGATCTATGTGGACATC 1293

RESULT 2
AY401137
LOCUS       AY401137               1296 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Pan troglodytes HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY401137
VERSION     AY401137.1  GI:39757126
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 1296)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1296)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
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Best Local Similarity:	98.84%	Mismatches:	5
Query Match:	98.73%	Indels:	0
DB:	9	Gaps:	0

US-10-735-014-83 (1-431) x AY401137 (1-1296)

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Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db         61 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAACAAGAGTCTAGAAGATGTTGTCATTGAC 120

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Db        361 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 420

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 480

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 540

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CACTTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 600

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAAGGCCATTCTCAGAGTTCACAGTTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 660

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 720

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCCAAAGCCCACCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 780

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACG 840

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 900

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCCTAGAAACCATA 960

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1020

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
              ||||||||||||||||||||||||||||||  ||||||||||||||||||  |||
Db       1021 CTTTCTATGTCAAATGTGGAGTCTTCCACTACGAATAAAACTGCTTCCTGGGAANGTAGG 1080

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAGGCCAGTCCAGGCAGTTCGTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1140

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1200

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db       1201 CTCGTCCTCCTGGGTAGAATCCTCTTGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1260

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
              |||||||||||||||||||||||||||||||||
Db       1261 GATTATTTGATCAATGGGATCTATGTGGACATC 1293
```

RESULT 3
CR621081

```
LOCUS       CR621081               1965 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI054YH07 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR621081
VERSION     CR621081.1  GI:50501888
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1965)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1965)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1965
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI054YH07"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN
```

Alignment Scores:

Pred. No.:	3.05e-156	Length:	1965
Score:	1831.00	Matches:	357
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	82.81%	Indels:	0
DB:	3	Gaps:	0

US-10-735-014-83 (1-431) x CR621081 (1-1965)

```
Qy         75 GlyAspLysAlaCysAsnLeuMetIlePheAspThrArgLysThrAlaArgGlnProAsn 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 GGGGACAAAGCATGTAACTTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAAC 206

Qy         95 CysTyrLeuPhePheCysProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeu 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 TGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTT 266

Qy        115 MetSerTyrArgIleIleThrAspPheProSerLeuThrArgAsnLeuProSerGlnGlu 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 ATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAG 326

Qy        135 LeuProGlnGluAspSerLeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAla 154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TTACCCCAGGAAGATTCTCTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCC 386

Qy        155 HisHisHisThrAspTyrSerLysProThrAspIleSerTrpArgAspThrLeuSerGln 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAG 446

Qy        175 LysPheGlySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGln 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AAGTTTGGATCCTCAGATCACTTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAG 506

Qy        195 LeuLeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGlu 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 CTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAA 566

Qy        215 IleAlaHisLeuLeuProGluAsnValSerAlaLeuProAlaThrValAlaValAlaSer 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ATAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCT 626

Qy        235 ProHisThrThrSerAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSerVal 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 CCACATACCACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTG 686

Qy        255 ThrProSerGlyThrSerGlnProGlnLeuAlaThrThrAlaProProValThrThrVal 274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 ACACCTTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTC 746

Qy        275 ThrSerGlnProProThrThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeu 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 ACTTCTCAGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTC 806

Qy        295 GlnAlaMetAlaThrThrAlaValLeuThrThrThrPheGlnAlaProThrAspSerLys 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 CAAGCAATGGCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAA 866

Qy        315 GlySerLeuGluThrIleProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsn 334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GGCAGCTTAGAAACCATACCGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAAT 926

Qy        335 ValTyrAsnProThrAlaLeuSerMetSerAsnValGluSerSerThrMetAsnLysThr 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 GTGTATAACCCTACTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACT 986

Qy        355 AlaSerTrpGluGlyArgGluAlaSerProGlySerSerSerGlnGlySerValProGlu 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GCTTCCTGGGAAGGTAGGGAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAA 1046

Qy        375 AsnGlnTyrGlyLeuProPheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyVal 394
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1047 AATCAGTACGGCCTTCCATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTC 1106

Qy        395 LeuPheLeuValIleGlyLeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArg 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1107 CTGTTCCTGGTGATAGGCCTCGTCCTCCTGGGTAGAATCCTCTCGGAATCACTCCGCAGG 1166

Qy        415 LysArgTyrSerArgLeuAspTyrLeuIleAsnGlyIleTyrValAspIle 431
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1167 AAACGTTACTCAAGACTGGATTATTTGATCAATGGGATCTATGTGGACATC 1217
```

```
RESULT 4
BQ424639
LOCUS       BQ424639                853 bp    mRNA    linear   EST 23-MAY-2002
DEFINITION  AGENCOURT_7896936 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6159709
            5', mRNA sequence.
ACCESSION   BQ424639
VERSION     BQ424639.1  GI:21119954
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 853)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13509  row: d  column: 14
            High quality sequence stop: 735.
FEATURES             Location/Qualifiers
     source          1. .853
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6159709"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
ORIGIN
```

```
Alignment Scores:
Pred. No.:              3.37e-115       Length:         853
Score:                  1376.00         Matches:        272
Percent Similarity:     99.28%          Conservative:   2
Best Local Similarity:  98.55%          Mismatches:     0
Query Match:            62.23%          Indels:         2
DB:                     5               Gaps:           0

US-10-735-014-83 (1-431) x BQ424639 (1-853)

Qy         73 IleSerGlyAspLysAlaCysAsnLeuMetIlePheAspThrArgLysThrAlaArgGln 92
              |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 ATTGCAGGGGACAAAGCATGTAACTTGATGATCTTCGACACTCGAAAAACAGCTAGACAA 76

Qy         93 ProAsnCysTyrLeuPhePheCysProAsnGluGluAlaCysProLeuLysProAlaLys 112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAA 136

Qy        113 GlyLeuMetSerTyrArgIleIleThrAspPheProSerLeuThrArgAsnLeuProSer 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 GGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGC 196

Qy        133 GlnGluLeuProGlnGluAspSerLeuLeuHisGlyGlnPheSerGlnAlaValThrPro 152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 CAAGAGTTACCCCAGGAAGATTCTCTCTTACATGGCCAATTTTCACAAGCAGTCACTCCC 256

Qy        153 LeuAlaHisHisHisThrAspTyrSerLysProThrAspIleSerTrpArgAspThrLeu 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 CTAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTT 316

Qy        173 SerGlnLysPheGlySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSer 192
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 TCTCAGAAGTTTGGATCCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGT 376

Qy        193 AlaGlnLeuLeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerSerAsp 212
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GCCCAGCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGAT 436

Qy        213 GlnGluIleAlaHisLeuLeuProGluAsnValSerAlaLeuProAlaThrValAlaVal 232
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CAAGAAATAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTT 496

Qy        233 AlaSerProHisThrThrSerAlaThrProLysProAlaThrLeuLeuProThrAsnAla 252
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 GCTTCTCCACATACCACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCT 556

Qy        253 SerValThrProSerGlyThrSerGlnProGlnLeuAlaThrThrAlaProProValThr 272
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 TCAGTGACACCTTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACC 616

Qy        273 ThrValThrSerGlnProProThrThrLeuIleSerThrValPheThrArgAlaAlaAla 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 ACTGTCACTTCTCAGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCT 676

Qy        293 ThrLeuGlnAlaMetAlaThrThrAlaValLeuThrThrThrPheGlnAlaProThrAsp 312
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 ACACTCCAAGCAATGGCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGAC 736

Qy        313 SerLysGlySerLeuGluThrIleProPheThrGluIleSerAsnLeuThrLeuAsnThr 332
                ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db        737 TCGAAAGGCAGCTTAGAAACCATACCGTTTACAGAAATCTCCCACTTAACTTTGAACACA 796

Qy        333 -GlyAsnValTyrAsn-ProThrAlaLeuSerMetSerAsnVal 346
                |||||||||||||| ||||||||||||||||||||||||||||
Db        797 GGGGAATGTGTATAACCCCTACTGCACTTTCTATGTCAAATGTG 840

RESULT 5
BX350141/c
LOCUS       BX350141                884 bp    mRNA    linear   EST 08-APR-2004
DEFINITION  BX350141 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI054YH07 3-PRIME, mRNA sequence.
ACCESSION   BX350141
VERSION     BX350141.1  GI:30365418
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 884)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            6656.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0BAI023ZA03_CS02129_1&c=6656.r

FEATURES             Location/Qualifiers
     source          1. .884
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI054YH07"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Alignment Scores:
Pred. No.:                4.53e-113      Length:          884
Score:                    1353.00        Matches:         283
Percent Similarity:       97.26%         Conservative:    1
Best Local Similarity:    96.92%         Mismatches:      8
Query Match:              61.19%         Indels:          3
DB:                       5              Gaps:            0

US-10-735-014-83 (1-431) x BX350141 (1-884)

Qy        125 SerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSerLeuLeuHisGly 144
                |||   |||||||||||   |||||||||||||||   ||||||||||||||||||||
Db        882 TCTTGGACCAGAAATTTGGCAAGCCAAGAGTTACCCAG-GAAGATTCTCTCTTACATGGC 824

Qy        145 GlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyrSerLysProThr 164
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        823 AA-TTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTATTCANAGCCCACC 765

Qy        165 AspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAspHisLeuGluLys 184
                 :::|||||||||||||||||   |||||||||||||   |||||||||||||||||||
Db        764 AATATCTCATGGAGAGACACACT-TCTCAGAAGTTTGATCCCTCAGATCACCTGGAGAAA 706

Qy        185 LeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGluLysGlyHisSer 204
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 CTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAAAAAGGCCATTCT 646

Qy        205 GlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuProGluAsnValSer 224
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 CAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCTGAAAATGTGAGT 586

Qy        225 AlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAlaThrProLysPro 244
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 GCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCTACTCCAAAGCCC 526

Qy        245 AlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSerGlnProGlnLeu 264
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCCCAGCCACAGCTG 466

Qy        265 AlaThrThrAlaProProValThrThrValThrSerGlnProProThrThrLeuIleSer 284
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCCACGACCCTCATTTCT 406

Qy        285 ThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThrAlaValLeuThr 304
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 ACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACAGCAGTTCTGACT 346

Qy        305 ThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIleProPheThrGlu 324
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 ACCACCTTTCAGGCACCTACGGACTCAAAAGGCAGCTTAGAAACCATACCGTTTACAGAA 286

Qy        325 IleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAlaLeuSerMetSer 344
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 ATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCACTTTCTATGTCA 226

Qy        345 AsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArgGluAlaSerPro 364
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 AATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGGGAGGCCAGTCCA 166

Qy        365 GlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuProPheGluLysTrp 384
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCATTTGAAAAATGG 106

Qy        385 LeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGlyLeuValLeuLeu 404
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 CTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGCCTCGTCCTCCTG 46

Qy        405 GlyArgIleLeuSerGluSerLeuArgArgLysArg 416
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Db         45 GGTAGAATCCTCTCGGAATCACTCCGCAGGAAACGT 10

RESULT 6
AL525434
LOCUS       AL525434               1050 bp    mRNA    linear   EST 24-MAR-2004
DEFINITION  AL525434 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC011YG07 5-PRIME, mRNA sequence.
ACCESSION   AL525434
VERSION     AL525434.3  GI:45700628
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1050)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:31063298.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            6656.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DC011AD04QP1&c=6656.r.
FEATURES             Location/Qualifiers
     source          1. .1050
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DC011YG07"
                     /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Alignment Scores:
Pred. No.:              3.05e-101      Length:         1050
Score:                  1225.00        Matches:        244
Percent Similarity:     93.13%         Conservative:   0
Best Local Similarity:  93.13%         Mismatches:     16
Query Match:            55.40%         Indels:         3
DB:                     1              Gaps:           1

US-10-735-014-83 (1-431) x AL525434 (1-1050)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 307

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 367

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 427

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTYAC 487

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        488 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 547

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        548 CCCAACGAGGAAGCCTGTYCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 607

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 667

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 727

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 787

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 847

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeu-LeuPr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        848 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCCTGCC 907

Qy        220 oGluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAl 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 TGAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACMACTC--GG 965

Qy        240 aThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSe 260
                  |||||||||          |||              |||   |||   |||
Db        966 YWATGCMAARCCSGCAMCCTTYTACCCM---CAATGCTTAGTGAMACCTYYTGGACTYCM 1022

Qy        260 rGln 261
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Db       1023 RCAA 1026

RESULT 7
AY401138
LOCUS       AY401138               1245 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Mus musculus HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY401138
VERSION     AY401138.1  GI:39757127
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1245)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1245)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .1245
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
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                     /db_xref="taxon:10090"
     gene            <1. .>1245
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ORIGIN

Alignment Scores:
Pred. No.:                1.09e-96        Length:          1245
Score:                    1176.50         Matches:         258
Percent Similarity:       68.91%          Conservative:    39
Best Local Similarity:    59.86%          Mismatches:      117
Query Match:              53.21%          Indels:          17
DB:                       9               Gaps:            6

US-10-735-014-83 (1-431) x AY401138 (1-1245)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              |||   |||   |||     ||||||   |||:::|||::::::|||   |||||||||
Db          1 ATGCTCTTCAGGGGAACC---AGCTTGGCTTACTCGTTGCTGGTCATTTCCTTCCTGACA 57

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
                 |||   ||||||   ||||||||||||   ||||||||||||||||||||||||||||
Db         58 CCAAGGTCGTCTGCTGGTCAGAACTGCCTCACCAAGAGTCTAGAAGACGTTGTCATTGAC 117

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||:::::   :::||||||
Db        118 ATCCAATCGTCGCTTTCAAAAGGCATTCGAGGCAATGAGCCCATACACGTGGCAACTCAG 177

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              |||||||||:::   :::|||||||||||||||:::|||:::||||||||||||||||||
Db        178 GAAGACTGTGTCGGTGCCTGCTGTTCAACAAAAGACATAGCAGGGGACAAGGCATGTAAT 237

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        238 TTGATGATCTTTGACACCCGGAAGACAGACAGACAGCCCAACTGCTACCTGTTTTTCTGT 297

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              |||:::|||:::|||||||||||||||||||||||||||||:::::|||||:::::::
Db        298 CCCAGCGAGGATGCCTGTCCGCTGAAGCCAGCCAAGGGCCTTGTGACCTACAGGCTCGTC 357

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
                 |||||||||      :::   |||         |||:::|||   |||   :::|||
Db        358 AGAGATTTTCCGCTGACCAGCGCTAATTCATCACTCCAACAGTTAACACAAGGAGAGTCT 417

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||              |||         ||||||                    |||
Db        418 CTCTTACTTGACCATTCGTCACCAGGAGCCACCCCTGGGTTTCGTACCCCAGCAGGTTAC 477

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
                 |||||||||   :::||||||   |||       |||   |||       :::
Db        478 CCAAAGCCCACCGGCCTGTCTTGGAGTGACGGATCTTCTCTGAAGTCCACAGCCCCCCTG 537

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              ||||||   |||       |||   ||||||   |||   ||||||         :::|||
Db        538 CACTTGCGCAAACACATCAAGGCTGATGAAACAAGCACGCAGCTC------CCTGAAGAA 591

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              |||   ||||||||||||   |||       |||:::   ::::::|||||||||||||||
Db        592 AAAAGCCATTCTCAGAGTTTACAGCTTCCCTCGGAACTAAAAATGGCTCATCTGCTCCCT 651

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
              :::   |||         |||   ||||||||||||||                ||||||
Db        652 AAAACTGTGCCGACTCCACCTACCACTGTAGCTGTGGCTCCCCTCCGTAACGTCTCTGCC 711

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              |||   |||||||||   ||||||   |||:::   |||||||||
Db        712 ACCCTGAAGCCTGCGCTTCTGTTG---ACCAGCATTTCAGTGACAGCTAAGACTTTGAAG 768

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              |||   :::   ||||||||||||   |||||||||||||||||||:::   |||
Db        769 CAGAAGGAG---GCCACCACAGCATCACCTGTCACCACCGTGACCTCGAAGCTCCCAGCA 825

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
                       ||||||   ||||||                          :::

Db        826 GTCCCTGGGTCTACAAGTTTTACA----------------CCCGTGGTTACACATCAG 867

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
              |||   ||||||   ||||||||||||   ||||||||||||||   |||||||||:::
Db        868 GCAGCTTTGACTAACACCTTTCAGGCACATACAGACTCCAAAGGCATCTTAGAAACAATG 927

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
              ||||||         |||   ||||||                        :::|||
Db        928 CCCTTTCAAGGAGGCTCTACGCTGACT----------------TCAGACCCGAGGCAC 969

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
                    |||       |||||||||       ||||||||||||||||||||   |||
Db        970 GGGAAAAGCTCAACCTCAGAGTCTTCCATTACAAACAAGACTGCTTCCTGGGAGGACAGG 1029

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
                    |||   ||||||:::|||           |||:::::::|||:::||||||
Db       1030 AGGGTCAGTGTAGGCAGCGCATCGCTGAACAAGGGTCCAAAAAGCCAGCATGGCCTTTCA 1089

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              ||||||||||||||||||||||||:::||||||   ||||||||||||||||||||||||
Db       1090 TTTGAGAAGTGGCTTCTCATTGGGACCCTCCTTTGTGGTGTTTTGTTTCTGGTAATAGGT 1149

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
              ||||||||||||||||||:::|||   |||:::||||||||||||||||||||||||||||
Db       1150 CTCGTCCTCTTGGGTAGGATGCTGGTTGAAGCCCTCCGTAGGAAACGGTATTCAAGACTT 1209

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
              |||||||||||||||||||||||||||||||
Db       1210 GACTACTTGATCAACGGGATCTATGTTGACATC 1242

RESULT 8
AK033526
LOCUS       AK033526               2235 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male colon cDNA, RIKEN full-length enriched
            library, clone:9030601P12 product:weakly similar to NT2RM1001115
            PROTEIN [Homo sapiens], full insert sequence.
ACCESSION   AK033526
VERSION     AK033526.1  GI:26329204
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
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  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2235)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .2235
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                     /strain="C57BL/6J"
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                     /db_xref="taxon:10090"
                     /clone="9030601P12"
                     /sex="male"
                     /tissue_type="colon"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     CDS             283. .1527
                     /note="unnamed protein product; putative
                     weakly similar to NT2RM1001115 PROTEIN [Homo sapiens]
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                     KPTGLSWSDRSSLKSTAPLHLRKHIKADETSMQLPEEKSHSQSLQLPSELKMAHLLPK
                     TVPTPPTTVAVAPLRNVSATLKPELLLTSISVTAKTLKQKEATTASPVTTVTSKLPGV
                     PGSTSFTPVVTHQAALTNTFQAHTDSKGILETMPFQGGSTLTSDPRHGKSSTSESSIT
                     NKTASWEDRRVSVGSASLNKGPKSQHGLSFEKWLLIGTLLCGVLFLVIGLVLLGRMLV
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                     /note="putative"
     polyA_site      2235
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ORIGIN

Alignment Scores:
Pred. No.:              3.46e-95        Length:         2235
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Score:                  1164.50         Matches:        258
Percent Similarity:     68.45%          Conservative:   37
Best Local Similarity:  59.86%          Mismatches:     119
Query Match:            52.67%          Indels:         17
DB:                     3               Gaps:           6

US-10-735-014-83 (1-431) x AK033526 (1-2235)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              |||   |||   |||       ||||||   |||:::|||::::::|||   |||||||||
Db        283 ATGCTCTTCAGGGGAACC---AGCTTGGCTTACTCGTTGCTGGTCATTTCCTTCCTGACA 339

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
                 |||   ||||||   ||||||||||||   |||||||||||||||||||||||||||||
Db        340 CCAAGGTCGTCTGCTGGTCAGAACTGCCTCACCAAGAGTCTAGAAGACGTTGTCATTGAC 399

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||||||||::::::   :::||||||
Db        400 ATCCAATCGTCGCTTTCAAAAGGCATTCGAGGCAATGAGCCCATACACTTGGCAACTCAG 459

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||   :::|||||||||||||||:::|||:::|||||||||||||||||||
Db        460 GAAGACTGTATCGGTGCCTGCTGTTCAACAAAAGACATAGCAGGGGACAAGGCATGTAAT 519

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Db        520 TTGATGATCTTTGACACCCGGAAGACAGACAGACAGCCCAACTGCTACCTGTTTTTCTGT 579

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              |||:::|||:::|||||||||||||||||||||||||||||:::::::||||||:::|||
Db        580 CCCAGCGAGGATGCCTGTCCGCTGAAGCCAGCCAAGGGCCTTGTGACCTACAGGCTCATC 639

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
                 |||||||||       :::   |||           |||:::|||   |||   :::
Db        640 AGAGATTTTCCGCTGACCAGCGCTAATTCATCACTCCAACAGTTAACACAAGGAGAGTTT 699

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||               |||           ||||||                   |||
Db        700 CTCTTACTTGACCATTCGTCACCAGGAGCCACCCCTGGGTTTCGTACCCCAGCAGGTTAC 759

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
                 |||||||||  :::||||||  |||       |||   |||       :::
Db        760 CCAAAGCCCACCGGCCTGTCTTGGAGTGACAGATCTTCTCTGAAGTCCACAGCCCCCCTG 819

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Db        820 CACTTGCGCAAACACATCAAGGCTGATGAAACAAGCATGCAGCTC------CCTGAAGAA 873

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db        874 AAAAGCCATTCTCAGAGTTTACAGCTTCCCTCAGAACTAAAAATGGCTCATCTGCTCCCT 933

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        934 AAAACTGTGCCGACTCCACCTACCACTGTAGCTGTGGCTCCCCTCCGTAACGTCTCTGCC 993

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
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Db        994 ACCCTGAAGCCTGAGCTTCTGTTG---ACCAGCATTTCAGTGACAGCTAAGACTTTGAAG 1050

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Db       1051 CAGAAGGAG---GCCACCACAGCATCACCTGTCACCACCGTGACCTCGAAGCTCCCAGGA 1107

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
                    ||||||   ||||||                              :::
Db       1108 GTCCCAGGGTCTACAAGTTTTACA------------------CCCGTGGTTACACATCAG 1149

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
              |||   ||||||   ||||||||||||   ||||||||||||||   |||||||||:::
Db       1150 GCAGCTTTGACTAACACCTTTCAGGCACATACAGACTCCAAAGGCATCTTAGAAACAATG 1209

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Db       1210 CCCTTTCAAGGAGGCTCTACGCTGACT-----------------TCAGACCCGAGGCAC 1251

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
                  |||       |||||||||       |||||||||||||||||||||   |||
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Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Db       1312 AGGGTCAGTGTAGGCAGCGCATCGCTGAACAAGGGTCCAAAAAGCCAGCATGGCCTTTCA 1371

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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Db       1432 CTCGTCCTCTTGGGTAGGATGCTGGTTGAAGCCCTCCGTAGGAAACGGTATTCAAGACTT 1491

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Db       1492 GACTACTTGATCAACGGGATCTATGTTGACATC 1524
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RESULT 9
AK018635
LOCUS AK018635 2265 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130017N16 product:weakly similar to NT2RM1001115 PROTEIN [Homo sapiens], full insert sequence.
ACCESSION AK018635
VERSION AK018635.1 GI:12858442
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2265)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.2. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.
FEATURES Location/Qualifiers
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/db_xref="taxon:10090"
/clone="9130017N16"
/sex="male"
/tissue_type="cecum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
CDS 262. .1506
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/codon_start=1
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DACPLKPAKGLVTYRLIRDFPLTSANSSLQQLTQGEFLLLDHSSPGATPGFRTPAGYP
KPTGLSWSDRSSLKSTAPLHLRKHIKADETSMQLPEEKSHSQSLQLPSELKMAHLLPK
TVPTPPTTVAVAPLRNVSATLKPELLLTSISVTAKTLKQKEATTASPVTTVTSKLPGV
PGSTSFTPVVTHQAALTNTFQAHTDSKGILETMPFQGGSTLTSDPRHGKSSTSESSIT
NKTASWEDRRVSVGSASLNKGPKSQHGLSFEKWLLIGTLLCGVLFLVIGLVLLGRMLV
EALRRKRYSRLDYLINGIYVDI"
ORIGIN

Alignment Scores:
Pred. No.: 3.54e-95 Length: 2265
Score: 1164.50 Matches: 258
Percent Similarity: 68.45% Conservative: 37

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Best Local Similarity:  59.86%          Mismatches:    119
Query Match:            52.67%          Indels:         17
DB:                     3               Gaps:           6

US-10-735-014-83 (1-431) x AK018635 (1-2265)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              |||   |||   |||       ||||||   |||:::|||::::::|||   |||||||||
Db        262 ATGCTCTTCAGGGGAACC---AGCTTGGCTTACTCGTTGCTGGTCATTTCCTTCCTGACA 318

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
                ||   ||||||   ||||||||||||   ||||||||||||||||||||||||||||||
Db        319 CCAAGGTCGTCTGCTGGTCAGAACTGCCTCACCAAGAGTCTAGAAGACGTTGTCATTGAC 378

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||||||::::::   :::||||||
Db        379 ATCCAATCGTCGCTTTCAAAAGGCATTCGAGGCAATGAGCCCATACACTTGGCAACTCAG 438

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||   :::|||||||||||||||:::|||:::||||||||||||||||||||
Db        439 GAAGACTGTATCGGTGCCTGCTGTTCAACAAAAGACATAGCAGGGGACAAGGCATGTAAT 498

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        499 TTGATGATCTTTGACACCCGGAAGACAGACAGACAGCCCAACTGCTACCTGTTTTTCTGT 558

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              |||:::|||:::|||||||||||||||||||||||||||||:::::|||||:::|||
Db        559 CCCAGCGAGGATGCCTGTCCGCTGAAGCCAGCCAAGGGCCTTGTGACCTACAGGCTCATC 618

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Db        619 AGAGATTTTCCGCTGACCAGCGCTAATTCATCACTCCAACAGTTAACACAAGGAGAGTTT 678

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||          |||         ||||||                      |||
Db        679 CTCTTACTTGACCATTCGTCACCAGGAGCCACCCCTGGGTTTCGTACCCCAGCAGGTTAC 738

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
               |||||||||   :::||||||   |||      |||   |||      :::
Db        739 CCAAAGCCCACCGGCCTGTCTTGGAGTGACAGATCTTCTCTGAAGTCCACAGCCCCCCTG 798

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              ||||||   |||       |||   ||||||   |||   ||||||         :::|||
Db        799 CACTTGCGCAAACACATCAAGGCTGATGAAACAAGCATGCAGCTC------CCTGAAGAA 852

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              |||   ||||||||||||   |||       |||::   ::::::|||||||||||||||
Db        853 AAAAGCCATTCTCAGAGTTTACAGCTTCCCTCAGAACTAAAAATGGCTCATCTGCTCCCT 912

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Db        913 AAAACTGTGCCGACTCCACCTACCACTGTAGCTGTGGCTCCCCTCCGTAACGTCTCTGCC 972

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              |||   ||||||       ||||||   |||:::   |||||||||
Db        973 ACCCTGAAGCCTGAGCTTCTGTTG---ACCAGCATTTCAGTGACAGCTAAGACTTTGAAG 1029

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              |||   :::   ||||||||||||   |||||||||||||||||||:::   |||
Db       1030 CAGAAGGAG---GCCACCACAGCATCACCTGTCACCACCGTGACCTCGAAGCTCCCAGGA 1086

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
                    ||||||   ||||||                              :::
Db       1087 GTCCCAGGGTCTACAAGTTTTACA----------------CCCGTGGTTACACATCAG 1128

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
              |||   ||||||   ||||||||||||   ||||||||||||   |||||||||:::
Db       1129 GCAGCTTTGACTAACACCTTTCAGGCACATACAGACTCCAAAGGCATCTTAGAAACAATG 1188

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Db       1189 CCCTTTCAAGGAGGCTCTACGCTGACT----------------TCAGACCCGAGGCAC 1230

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Db       1231 GGGAAAAGCTCAACCTCAGAGTCTTCCATTACAAACAAGACTGCTTCCTGGGAGGACAGG 1290

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
                    |||   ||||||:::|||             |||:::::|||:::||||||
Db       1291 AGGGTCAGTGTAGGCAGCGCATCGCTGAACAAGGGTCCAAAAAGCCAGCATGGCCTTTCA 1350

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              ||||||||||||||||||||||||:::||||||   ||||||||||||||||||||||||
Db       1351 TTTGAGAAGTGGCTTCTCATTGGGACCCTCCTTTGTGGTGTTTTGTTTCTGGTAATAGGT 1410

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
              ||||||||||||||||||:::|||   |||:::||||||||||||||||||||||||||||
Db       1411 CTCGTCCTCTTGGGTAGGATGCTGGTTGAAGCCCTCCGTAGGAAACGGTATTCAAGACTT 1470

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
              |||||||||||||||||||||||||||||||
Db       1471 GACTACTTGATCAACGGGATCTATGTTGACATC 1503

RESULT 10
AK046837
LOCUS       AK046837               2265 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 10 days neonate medulla oblongata cDNA, RIKEN
            full-length enriched library, clone:B830022E21 product:weakly
            similar to NT2RM1001115 PROTEIN [Homo sapiens], full insert
            sequence.
ACCESSION   AK046837
VERSION     AK046837.1  GI:26338441
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
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REFERENCE 6 (bases 1 to 2265)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers
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/note="putative"

ORIGIN

Alignment Scores:

Pred. No.:	3.54e-95	Length:	2265
Score:	1164.50	Matches:	258
Percent Similarity:	68.45%	Conservative:	37
Best Local Similarity:	59.86%	Mismatches:	119
Query Match:	52.67%	Indels:	17
DB:	3	Gaps:	6

US-10-735-014-83 (1-431) x AK046837 (1-2265)

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Db        317 CCAAGGTCGTCTGCTGGTCAGAACTGCCTCACCAAGAGTCTAGAAGACGTTGTCATTGAC 376

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60

Db        377 ATCCAATCGTCGCTTTCAAAAGGCATTCGAGGCAATGAGCCCATACACTTGGCAACTCAG 436

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Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100

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Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220

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Db       1229 GGGAAAAGCTCAACCTCAGAGTCTTCCATTACAAACAAGACTGCTTCCTGGGAGGACAGG 1288

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RESULT 11
AK018660
LOCUS AK018660 2286 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130403P13 product:weakly similar to NT2RM1001115 PROTEIN [Homo sapiens], full insert sequence.
ACCESSION AK018660
VERSION AK018660.1 GI:12858477
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2286)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.2. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.
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CDS 284. .1528
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weakly similar to NT2RM1001115 PROTEIN [Homo sapiens]
(SPTR|Q9NW60, evidence: FASTY, 58.3%ID, 96.7%length,
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ORIGIN

Alignment Scores:

Pred. No.:	3.59e-95	Length:	2286
Score:	1164.50	Matches:	258
Percent Similarity:	68.45%	Conservative:	37
Best Local Similarity:	59.86%	Mismatches:	119
Query Match:	52.67%	Indels:	17
DB:	3	Gaps:	6

US-10-735-014-83 (1-431) x AK018660 (1-2286)

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Qy       301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Qy       361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Qy       401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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RESULT 12
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DEFINITION Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030619P12 product:weakly similar to NT2RM1001115 PROTEIN [Homo sapiens], full insert sequence.
ACCESSION AK033557
VERSION AK033557.1 GI:26329236
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2375)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,

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            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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ORIGIN

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Pred. No.:              3.82e-95        Length:         2375
Score:                  1164.50         Matches:        258
Percent Similarity:     68.45%          Conservative:   37
Best Local Similarity:  59.86%          Mismatches:     119
Query Match:            52.67%          Indels:         17
DB:                     3               Gaps:           6

US-10-735-014-83 (1-431) x AK033557 (1-2375)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              |||  |||  |||    ||||||  |||:::|||::::::|||  |||||||||
Db        372 ATGCTCTTCAGGGGAACC---AGCTTGGCTTACTCGTTGCTGGTCATTTCCTTCCTGACA 428

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
                ||   ||||||  ||||||||||||  ||||||||||||||||||||||||||||||
Db        429 CCAAGGTCGTCTGCTGGTCAGAACTGCCTCACCAAGAGTCTAGAAGACGTTGTCATTGAC 488

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||||||::::::   :::||||||

Db        489 ATCCAATCGTCGCTTTCAAAAGGCATTCGAGGCAATGAGCCCATACACTTGGCAACTCAG 548

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||  :::|||||||||||||||:::|||:::|||||||||||||||||||

Db        549 GAAGACTGTATCGGTGCCTGCTGTTCAACAAAAGACATAGCAGGGGACAAGGCATGTAAT 608

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||

Db        609 TTGATGATCTTTGACACCCGGAAGACAGACAGACAGCCCAACTGCTACCTGTTTTTCTGT 668

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              |||:::|||:::|||||||||||||||||||||||||||||:::::|||||:::|||

Db        669 CCCAGCGAGGATGCCTGTCCGCTGAAGCCAGCCAAGGGCCTTGTGACCTACAGGCTCATC 728

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
                |||||||||      :::   |||         |||:::|||   |||   :::

Db        729 AGAGATTTTCCGCTGACCAGCGCTAATTCATCACTCCAACAGTTAACACAAGGAGAGTTT 788

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||          |||         ||||||                      |||

Db        789 CTCTTACTTGACCATTCGTCACCAGGAGCCACCCCTGGGTTTCGTACCCCAGCAGGTTAC 848

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              |||||||||  :::||||||  |||     |||   |||      :::

Db        849 CCAAAGCCCACCGGCCTGTCTTGGAGTGACAGATCTTCTCTGAAGTCCACAGCCCCCCTG 908

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              ||||||  |||     |||  ||||||  |||  ||||||         :::|||

Db        909 CACTTGCGCAAACACATCAAGGCTGATGAAACAAGCATGCAGCTC------CCTGAAGAA 962

Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              |||  ||||||||||||  |||      |||:::  ::::::|||||||||||||||

Db        963 AAAAGCCATTCTCAGAGTTTACAGCTTCCCTCAGAACTAAAAATGGCTCATCTGCTCCCT 1022

Qy        221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
              :::  |||        |||  ||||||||||||||||                ||||||

Db       1023 AAAACTGTGCCGACTCCACCTACCACTGTAGCTGTGGCTCCCCTCCGTAACGTCTCTGCC 1082

Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              |||  ||||||      ||||||  |||:::  |||||||||

Db       1083 ACCCTGAAGCCTGAGCTTCTGTTG---ACCAGCATTTCAGTGACAGCTAAGACTTTGAAG 1139

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
              |||  :::  ||||||||||||  ||||||||||||||||||:::  |||

Db       1140 CAGAAGGAG---GCCACCACAGCATCACCTGTCACCACCGTGACCTCGAAGCTCCCAGGA 1196

Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
                    ||||||  ||||||                        :::

Db       1197 GTCCCAGGGTCTACAAGTTTTACA----------------CCCGTGGTTACACATCAG 1238

Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
              |||  ||||||  ||||||||||||  ||||||||||||||  |||||||||:::

Db       1239 GCAGCTTTGACTAACACCTTTCAGGCACATACAGACTCCAAAGGCATCTTAGAAACAATG 1298

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
              ||||||          |||  ||||||                        :::|||

Db       1299 CCCTTTCAAGGAGGCTCTACGCTGACT----------------TCAGACCCGAGGCAC 1340

Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
                  |||      |||||||||      ||||||||||||||||||||  |||

Db       1341 GGGAAAAGCTCAACCTCAGAGTCTTCCATTACAAACAAGACTGCTTCCTGGGAGGACAGG 1400

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
                |||   ||||||:::|||          |||::::::|||:::|||||

Db       1401 AGGGTCAGTGTAGGCAGCGCATCGCTGAACAAGGGTCCAAAAAGCCAGCATGGCCTTTCA 1460

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              ||||||||||||||||||||:::||||||  ||||||||||||||||||||||||||||

Db       1461 TTTGAGAAGTGGCTTCTCATTGGGACCCTCCTTTGTGGTGTTTTGTTTCTGGTAATAGGT 1520

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
              ||||||||||||||||:::|||   |||:::||||||||||||||||||||||||||||

Db       1521 CTCGTCCTCTTGGGTAGGATGCTGGTTGAAGCCCTCCGTAGGAAACGGTATTCAAGACTT 1580
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Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
              |||||||||||||||||||||||||||||||||
Db       1581 GACTACTTGATCAACGGGATCTATGTTGACATC 1613

RESULT 13
CV024215
LOCUS       CV024215                623 bp    mRNA    linear   EST 20-AUG-2004
DEFINITION  1439 Full Length cDNA from the Mammalian Gene Collection Homo
            sapiens cDNA 5' similar to BC032998, mRNA sequence.
ACCESSION   CV024215
VERSION     CV024215.1  GI:51482047
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 623)
  AUTHORS   Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
            Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
            Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
            Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
            Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M.
  TITLE     Human ORFeome Version 1.1: a Platform for Reverse Proteomics
  JOURNAL   Genome Res. (2004) In press
COMMENT     Contact: Vidal M
            Marc Vidal Laboratory
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc_Vidal@dfci.harvard.edu
            ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
            results from a PCR reaction using an MGC full-length cDNA as
            template DNA and ORF specific primers
            PCR PRimers
            FORWARD: ATGTTCTTCGGGGGAGAAGGGAG
            BACKWARD: TAGATGTCCACATAGATCCCATT
            Insert Length: 623   Std Error: 122.00
            Plate: 11036  row: 12  column: E
            Seq primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC
            High quality sequence start: 94
            High quality sequence stop: 622
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .623
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="mixed"
                     /clone_lib="Full Length cDNA from the Mammalian Gene
                     Collection"
                     /note="Vector: mixed; The ORFs were PCR amplified from the
                     MGC (Mammalian Gene Collection) as of April 2004 and
                     cloned by recombinational Gateway cloning into pDONR223
                     Donor vector. Reference : MGC (Mammalian Gene Collection)
                     Program Team, Generation and Initial Analysis of more than
                     15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
                     2002, 99(26), 16899-16903"
ORIGIN

Alignment Scores:
Pred. No.:              3.01e-88        Length:         623
Score:                  1079.00         Matches:        204
Percent Similarity:     99.03%          Conservative:   1
Best Local Similarity:  98.55%          Mismatches:     2
Query Match:            48.80%          Indels:         0
DB:                     7               Gaps:           0

US-10-735-014-83 (1-431) x CV024215 (1-623)

Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          1 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 60

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         61 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 120

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||

Db        121 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCATATATACTTCAACTCAA 180

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        181 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 240

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        241 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT 300

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        301 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 360

Qy        121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||

Db        361 ACAGATTTTCCATCTTTGACCATAAATTTGCCAAGCCAAGAGTTACCCCAGGAAGATTCT 420

Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        421 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 480

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        481 TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 540

Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||

Db        541 CACTTGGAGAAACTATTTAAGATGGATGAAGCATGTGCCCAGCTCCTTGCTTATAAGGAA 600

Qy        201 LysGlyHisSerGlnSerSer 207
              |||||||||||||||||||
Db        601 AAAGGGCATTCTCAGAGTTCA 621

RESULT 14
CF595929
LOCUS       CF595929                753 bp    mRNA    linear   EST 26-SEP-2003
DEFINITION  AGENCOURT_15668985 NCI_CGAP_St3 Homo sapiens cDNA clone
            IMAGE:30703562 5', mRNA sequence.
ACCESSION   CF595929
VERSION     CF595929.1  GI:36351906
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 753)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Arnold Schwartz, MD, PhD
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDCM251  row: d  column: 03
            High quality sequence stop: 540.
FEATURES             Location/Qualifiers
```

```
     source          1. .753
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30703562"
                     /tissue_type="Stomach, adenocarcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_St3"
                     /note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
                     Site_2: SfiI (ggccgcctcggcc); Library is oligo-dT primed
                     and directionally cloned. 5' and 3' adaptors were used in
                     cloning as follows: 5' adaptor sequence:
                     5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C, G, or T). Average insert size 1.30
                     kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech Laboratories (Palo Alto,
                     CA)."
ORIGIN

Alignment Scores:
Pred. No.:                1.18e-86        Length:          753
Score:                    1063.00         Matches:         219
Percent Similarity:       97.77%          Conservative:    0
Best Local Similarity:    97.77%          Mismatches:      3
Query Match:              48.08%          Indels:          2
DB:                       7               Gaps:            0

US-10-735-014-83 (1-431) x CF595929 (1-753)

Qy        175 LysPheGlySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGln 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 AAGTTTGGATCCTCAGATCACTTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAG 64

Qy        195 LeuLeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGlu 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 CTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAA 124

Qy        215 IleAlaHisLeuLeuProGluAsnValSerAlaLeuProAlaThrValAlaValAlaSer 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 ATAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCT 184

Qy        235 ProHisThrThrSerAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSerVal 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 CCACATACCACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTG 244

Qy        255 ThrProSerGlyThrSerGlnProGlnLeuAlaThrThrAlaProProValThrThrVal 274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 ACACCTTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTC 304

Qy        275 ThrSerGlnProProThrThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeu 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 ACTTCTCAGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTC 364

Qy        295 GlnAlaMetAlaThrThrAlaValLeuThrThrThrPheGlnAlaProThrAspSerLys 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 CAAGCAATGGCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAA 424

Qy        315 GlySerLeuGluThrIleProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsn 334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 GGCAGCTTAGAAACCATACCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAAT 484

Qy        335 ValTyrAsnProThrAlaLeuSerMetSerAsnValGluSerSerThrMetAsnLysThr 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 GTGTATAACCCTACTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACT 544

Qy        355 AlaSerTrpGluGlyArgGluAlaSerProGlySerSerSerGlnGlySerValProGlu 374
              ||||||   ||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        545 GCTTCCTGNGAAGGTAGGGAGGCCAGTCCAGGCAGTTTCTCCCAGGGCAGTGTTCCAGAA 604

Qy        375 AsnGlnTyrGlyLeuProPheGluLysTrpLeuLeuIleGlySerLeu-LeuPhe-GlyV 394
              |||||||||   ||||||||||||||||||||||||||||||||||| |||||| ||||

Db        605 AATCAGTACCGCCTTCCATTTGAAAAATGGCTTCTTATCGGGTCCCTGCCTCTTTGGGTG 664

Qy        394 alLeuPhe 396
              ||||||||
Db        665 TCCTGTTC 672

RESULT 15
AK002644
LOCUS       AK002644               2227 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male kidney cDNA, RIKEN full-length enriched
            library, clone:0610017A09 product:weakly similar to NT2RM1001115
            PROTEIN [Homo sapiens], full insert sequence.
ACCESSION   AK002644
VERSION     AK002644.1  GI:12832780
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2227)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
            Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
            Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
            Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
            Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
            Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
```

Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT Please visit our web site (http://genome.gsc.riken.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0. Second strand cDNA was prepared with the primer adapter of sequence[5' GAGAGAGAGAAGGATCCAAGAGCTCAATTAATTTAATTAAACCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

FEATURES Location/Qualifiers

source 1. .2227
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:0610017A09"
/db_xref="taxon:10090"
/clone="0610017A09"
/sex="male"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"

misc_feature 1. .2227
/note="weakly similar to NT2RM1001115 PROTEIN [Homo sapiens] (SPTR|Q9NW60, evidence: FASTY, 58.3%ID, 96.7%length, match=1104)"

ORIGIN

Alignment Scores:

Pred. No.:	2.9e-85	Length:	2227
Score:	1056.00	Matches:	248
Percent Similarity:	66.36%	Conservative:	38
Best Local Similarity:	57.54%	Mismatches:	128
Query Match:	47.76%	Indels:	20
DB:	3	Gaps:	6

US-10-735-014-83 (1-431) x AK002644 (1-2227)

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Qy          1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20
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Db        280 ATGCTCTTCAGGGGAACC---AGCTTGGCTTACTCGTTGCTGGTCATTTCCTTCCTGACA 336

Qy         21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
                 |||   ||||||   ||||||||||||   ||||||||||||||||||||||||||||
Db        337 CCAAGGTCGTCTGCTGGTCAGAACTGCCTCACCAAGAGTCTAGAAGACGTTGTCATTGAC 396

Qy         41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
              ||||||||||||||||||||||||||||||||||||||||||::::::   :::||||||
Db        397 ATCCAATCGTCGCTTTCAAAAGGCATTCGAGGCAATGAGCCCATACACTTGGCAACTCAG 456

Qy         61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
              ||||||||||||   :::|||||||||||||||:::|||:::||||||||||||||||||
Db        457 GAAGACTGTATCGGTGCCTGCTGTTCAACAAAAGACATAGCAGGGGACAAGGCATGTAAT 516

Qy         81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        517 TTGATGATCTTTGACACCCGGAAGACAGACAGACAGCCCAACTGCTACCTGTTTTTCTGT 576

Qy        101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Qy        141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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Db        697 CTCTTACTTGACCATTCGTCACCAGGAGCCACCCCTGGGTTTCGTACCCCAGCAGGTTAC 756

Qy        161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Qy        181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
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Qy        201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
              |||   ||||||||||||   |||       |||:::   ::::::|||||||||||||||
Db        871 AAAAGCCATTCTCAGAGTTTACAGCTTCCCTCAGAACTAAAAATGGCTCATCTGCTCCCT 930

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Qy        241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
              |||   ||||||       ||||||   |||:::   |||||||||
Db        991 ACCCTGAAGCCTGAGCTTCTGTTG---ACCAGCATTTCAGTGACAGCTAAGACTTTGAAG 1047

Qy        261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Qy        281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Qy        301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db       1147 GCAGCTTTGACTAACACCTTTCAGGCACATACAGACTCCAAAGGCATCTTAGAAACAATG 1206

Qy        321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Qy        341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
                    |||       |||||||||       ||||||||||||||||||||   |||
Db       1249 GGGAAAAGCTCAACCTCAGAGTCTTCCATTACAAACAAGACTGCTTCCTGGGAGGACAGG 1308

Qy        361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
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Db       1309 AGGGTCAGTGTAGGCAGCGCATCGCTGAACAAGGGTCCAAAAAGCCAGCATGT-CTTACA 1367

Qy        381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
              |||||||||       |||||||||   :::|||       |||||||||       :::
Db       1368 TTTGAGAAGGG-TCTCTCATCGGACCCATCCTTGG-TGTGTATTGTTCTGGTAAGTAGCT 1425

Qy        401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
              |||   ||||||||||||:::|||   |||:::||||||||||||||||||||||||||||
Db       1426 CTCGCTCTCTTGGGTAGGATGCTGGTTGAAGCCCTCCGTAGGAAACGGTATTCAAGACTT 1485

Qy        421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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Search completed: April 27, 2005, 00:58:02
Job time : 3367 secs